

74617

From: Schultz, James
Sent: Thursday, August 29, 2002 4:48 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search for 8 cases

Hello,
I have 8 cases that all require identical sequence searches (the only variables being the SEQ ID to be searched, the length of the target, and the length of the hit returned). If it suits you, I would like to condense all requests to this email. If you prefer 8 different emails, please respond and I'll split the requests up.

For all 8 cases, I need a length limited search against each of the sequences listed below. The maximum length of each hit to be returned follows each SEQ ID.

CASE 10/019,470,	SEQ ID. NO 1, 2828 nt long,	max return hit length, 30 nucleotides
CASE 10/049,743,	SEQ ID. NO 1, 3868 nt long,	max return hit length, 30 nucleotides
CASE 10/154,708,	SEQ ID. NO 3, 1834 nt long,	max return hit length, 30 nucleotides
CASE 10/177,554	SEQ ID. NO 4, 1321 nt long,	max return hit length, 80 nucleotides
CASE 10/174,456,	SEQ ID. NO 4, 2724 nt long,	max return hit length, 80 nucleotides
CASE 10/174,128,	SEQ ID. NO 4, 755 nt long,	max return hit length, 80 nucleotides
CASE 10/189,268,	SEQ ID. NO 4, 1395 nt long,	max return hit length, 80 nucleotides
CASE 10/178,258,	SEQ ID. NO 4, 1550 nt long,	max return hit length, 80 nucleotides

Thanks, Doug

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Mail: CM1 11E12

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Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

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AUG 30 2002
STIC/BIO/CHM. DIVISION
(STIC/6B.0)

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 8/31/02
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: Q6
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 23:42:49 ; Search time 3483.49 Seconds
(without alignments)
16988.780 Million cell updates/sec

Title: US-10-019-470-1
Perfect score: 2828
Sequence: 1 gttgaagctcctggcgagg.....aaagtccaattccaagga 2828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues 524256
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:**

- 1: gb_ba:**
- 2: gb_htg:**
- 3: gb_in:**
- 4: gb_om:**
- 5: gb_ov:**
- 6: gb_pat:**
- 7: gb_ph:**
- 8: gb_pl:**
- 9: gb_pr:**
- 10: gb_ro:**
- 11: gb_sts:**
- 12: gb_sy:**
- 13: gb_un:**
- 14: gb_vi:**
- 15: em_ba:**
- 16: em_fun:**
- 17: em_hum:**
- 18: em_in:**
- 19: em_mu:**
- 20: em_om:**
- 21: em_or:**
- 22: em_ov:**
- 23: em_pat:**
- 24: em_ph:**
- 25: em_pl:**
- 26: em_ro:**
- 27: em_sts:**
- 28: em_un:**
- 29: em_vi:**
- 30: em_htg_hum:**
- 31: em_htg_inv:**
- 32: em_htg_other:**
- 33: em_htgo_inv:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	20.6	0.7	21	6	AX096602	Sequence
2	20.6	0.7	21	6	AX096603	Sequence
3	20.6	0.7	21	6	AX096604	Sequence
4	20.6	0.7	21	6	AX096605	Sequence
5	20.6	0.7	21	6	AX096606	Sequence
6	20.6	0.7	21	6	AX153968	Sequence
7	20.6	0.7	21	6	AX153969	Sequence
8	20.6	0.7	21	6	AX153970	Sequence
9	20.6	0.7	21	6	AX153971	Sequence
10	20.6	0.7	21	6	AX153972	Sequence
11	20.6	0.7	21	6	AX153973	Sequence
12	20.6	0.7	21	6	AX153974	Sequence
13	19.6	0.7	30	6	A17675	Nucleotide
14	19.6	0.7	30	6	AR016317	Sequence
15	19	0.7	29	6	AX306690	Sequence
16	18.8	0.7	24	6	AX292738	Sequence
17	18.2	0.6	28	6	AX052812	Sequence
18	18	0.6	30	6	A98653	Sequence
19	17.8	0.6	21	6	AR067354	Sequence
20	17.8	0.6	21	6	AX094946	Sequence
21	17.8	0.6	25	6	AR078206	Sequence
22	17.8	0.6	25	6	AR081978	Sequence
23	17.8	0.6	23	6	AR139684	Sequence
24	17.8	0.6	27	6	A56639	Sequence
25	17.8	0.6	27	6	A80360	Sequence
26	17.8	0.6	27	6	AR111763	Sequence
27	17.8	0.6	28	6	AR137966	Sequence
28	17.6	0.6	24	6	AX299470	Sequence
29	17.6	0.6	30	6	A17666	Nucleotide
30	17.6	0.6	30	6	AR016319	Sequence
31	17.6	0.6	30	6	AR109703	Sequence
32	17.4	0.6	20	6	AX297371	Sequence
33	17.4	0.6	29	6	AX116714	Sequence
34	17.4	0.6	29	6	AX180734	Sequence
35	17.4	0.6	29	6	AX180857	Sequence
36	17.2	0.6	25	6	AR146793	Sequence
37	17.2	0.6	26	6	I69201	Sequence
38	17.2	0.6	27	6	AX197119	Sequence
39	17.2	0.6	27	6	E12911	PCR primer
40	17.2	0.6	29	6	AR035693	Sequence
41	17.2	0.6	29	6	AX337976	Sequence
42	17.2	0.6	29	6	E13899	PCR primer
43	17.2	0.6	30	6	A26599	Human inter
44	17.2	0.6	30	6	A87724	Sequence
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ALIGNMENTS

RESULT 1	AX096602	Sequence 1780 from Patent WO0118250.	21 bp	DNA	linear	PAT 30-MAR-2001
LOCUS	AX096602	Sequence 1780 from Patent WO0118250.	21 bp	DNA	linear	PAT 30-MAR-2001
DEFINITION	AX096602	Sequence 1780 from Patent WO0118250.	21 bp	DNA	linear	PAT 30-MAR-2001
ACCESSION	AX096602	Sequence 1780 from Patent WO0118250.	21 bp	DNA	linear	PAT 30-MAR-2001
VERSION	AX096602.1	GI:13512856	21 bp	DNA	linear	PAT 30-MAR-2001
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 21) Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and McCarthy, J.J.					
TITLE	Single nucleotide polymorphisms in genes					
JOURNAL	Patent: WO 0118250-A 1780 15-MAR-2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)					
FEATURES	Location/Qualifiers					
source	1..21					
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	/db_xref="taxon:9606"					
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ORIGIN

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Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy / 1123 agctgaatgatactcacctc 1143
|||||:|||||:|||||:|||||
Db 1 AGCTGAATGAYACTCACCTC 21

RESULT 2

AX096603
LOCUS AX096603 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1781 from Patent WO0118250.
ACCESSION AX096603
VERSION AX096603.1 GI:13512857
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthy,J.J.

TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1781 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)

FEATURES
source Location/Qualifiers

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/db_xref="taxon:9606"

BASE COUNT 5 a 5 c 6 g 4 t 1 others
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Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1978 agctgatcactcagtcgagc 1998
|||||:|||||:|||||:|||||
Db 1 AGCTGATCACYTCAGTGCAG 21

RESULT 3

AX096604
LOCUS AX096604 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1782 from Patent WO0118250.
ACCESSION AX096604
VERSION AX096604.1 GI:13512858
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthy,J.J.

TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1782 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)

FEATURES
source Location/Qualifiers

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/db_xref="taxon:9606"

BASE COUNT 9 a 3 c 4 g 4 t 1 others
ORIGIN

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Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1873 tgtacaaccgcattaaagaag 1893
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Db 1 TGTACAACCGYATTAGAAG 21

RESULT 4

AX096605
LOCUS AX096605 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1783 from Patent WO0118250.
ACCESSION AX096605
VERSION AX096605.1 GI:13512859
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthy,J.J.

TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1783 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)

FEATURES
source Location/Qualifiers

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BASE COUNT 7 a 3 c 4 g 6 t 1 others
ORIGIN

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Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2027 aagcaagttgaagtcattc 2047
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Db 1 AAGCAAGTTGRAAGTCATCTT 21

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AX096606
LOCUS AX096606 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1784 from Patent WO0118250.
ACCESSION AX096606
VERSION AX096606.1 GI:13512860
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthy,J.J.

TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1784 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)

FEATURES
source Location/Qualifiers

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BASE COUNT 5 a 3 c 8 g 4 t 1 others
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Query Match 0.7%; Score 20.6; DB 6; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1377 gatgtgacctctgagaag 1397
Db 1 GATGTGGACCTCTGAGAAG 21

RESULT 6
AX153968
LOCUS AX153968 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 66 from Patent WO0138576.
ACCESSION AX153968
VERSION AX153968.1 GI:14535582
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 66 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 7 a 7 c 3 t 1 others
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1218 aaccgaagaccttcgctac 1238
Db 1 AACCAGAGASCTTCGCTAC 21

RESULT 7
AX153969
LOCUS AX153969 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 67 from Patent WO0138576.
ACCESSION AX153969
VERSION AX153969.1 GI:14535583
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 67 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 4 a 7 c 6 g 3 t 1 others
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1706 cctccgggaactcgccaagt 1726
Db 1 CCTCCGGGAAMTCGCCAGGT 21

RESULT 8
AX153970
LOCUS AX153970 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 68 from Patent WO0138576.
ACCESSION AX153970
VERSION AX153970.1 GI:14535584
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 68 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 6 a 4 c 5 g 5 t 1 others
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 21;
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Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2003 ggtgaacaatgacctatggt 2023
Db 1 GGTGAACAATRACCCCTATGGT 21

RESULT 9
AX153971
LOCUS AX153971 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 69 from Patent WO0138576.
ACCESSION AX153971
VERSION AX153971.1 GI:14535585
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 69 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 4 a 7 c 7 g 2 t 1 others
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Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2119 ctgcaggcaccgaagcctcgg 2139
Db 1 CTGCAGGCACYGAGCCTCGG 21

RESULT 10
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LOCUS AX153972 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 70 from Patent WO0138576.
ACCESSION AX153972
VERSION AX153972.1 GI:14535586
KEYWORDS human.
SOURCE Homo sapiens

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 70 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 6 a 3 c 6 g 5 t 1 others
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2269 ttgctgcttggacaagaag 2289
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Db 1 TGGCTGCTTTRGACAGAAG 21

RESULT 11
AX153973 21 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 71 from Patent WO0138576.
ACCESSION AX153973
VERSION AX153973.1 GI:14535587
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 71 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 8 a 3 c 8 g 1 t 1 others
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2279 ggacaagaagggtacagagc 2299
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Db 1 GGACAAGAAAGGTACGAGC 21

RESULT 12
AX153974 21 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 72 from Patent WO0138576.
ACCESSION AX153974
VERSION AX153974.1 GI:14535588
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 72 31-MAY-2001;

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
Location/Qualifiers
source 1..21
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Query Match 0.7%; Score 20.6; DB 6; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.8e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2350 ttgacaatggctttttcttc 2370
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Db 1 TTGACAATGGVTTTTTCTC 21

RESULT 13
AL17675 30 bp DNA linear PAT 19-APR-1994
LOCUS
DEFINITION Nucleotide sequence 10 from patent number EP0461045.
ACCESSION AL17675
VERSION AL17675.1 GI:513934
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Guesdon,J.-L. and Thierry,D.
TITLE Specific detection of mycobacterium tuberculosis
JOURNAL Patent: EP 0461045-A 10 11-DEC-1991;
INSTITUT PASTEUR
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ORIGIN

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Best Local Similarity 84.6%; Pred. No. 7.9e+06;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2185 ggaccatggatgggcccaatgtgaa 2210
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Db 4 GGACCATGGAGTGGCCATCGTGAA 29

RESULT 14
AR016317 30 bp DNA linear PAT 05-DEC-1998
LOCUS
DEFINITION Sequence 11 from patent US 5776693.
ACCESSION AR016317
VERSION AR016317.1 GI:3972594
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Guesdon,J.-L. and Thierry,D.
TITLE Specific detection of the mycobacterium tuberculosis
JOURNAL Patent: US 5776693-A 11 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
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ORIGIN

Query Match 0.7%; Score 19.6; DB 6; Length 30;
Best Local Similarity 84.6%; Pred. No. 7.9e+06;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2185 ggaccatggatgggccaatgtgaa 2210
 |||||
 Db 4 GGACCATGGAGGTGGCCATCGTGAA 29

RESULT 15

AX306690
 LOCUS AX306690 29 bp DNA linear PAT 11-DEC-2001
 DEFINITION Sequence 8 from Patent WO0187925.
 ACCESSION AX306690
 VERSION AX306690.1 GI:17645857

KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.

REFERENCE
 1 (sites)
 Rosendahl, M.S., Cox, G.N. and Doherty, D.H.
 Methods for refolding proteins containing free cysteine residues
 Patent: WO 0187925-A 8 22-NOV-2001;
 Bolder Biotechnology, Inc. (US)

FEATURES
 Location/Qualifiers

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 /db_xref="taxon:32630"
 /note="primer"

BASE COUNT 4 a 13 c 9 g 3 t
 ORIGIN

Query Match 0.7%; Score 19; DB 6; Length 29;

Best Local Similarity 81.5%; Pred. No. 1e+07;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 788 gccatatgacaccccgagcccgcta 814
 |||||
 Db 2 GCCATATGACCCCGCTGGCCCGGCCA 28

Search completed: September 7, 2002, 02:03:23
 Job time: 8434 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 00:22:14 ; Search time 306.44 Seconds
(without alignments)
15844.648 Million cell updates/sec

Title: US-10-019-470-1

Perfect score: 2828

Sequence: 1 gttgaagctctcgcgcgg.....aaagtgtcaattccaagga 2828

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1662488

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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4: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT.*
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23: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	1.0	27	AA14004	Human liver glyco
2	21	0.7	21	AA14002	Human liver glyco
3	21	0.7	21	AA14003	Human liver glyco
4	21	0.7	21	AAH62165	Phosphorylaes gly
5	21	0.7	21	AAH62166	Phosphorylaes gly
6	21	0.7	21	AAH62167	Phosphorylaes gly
7	21	0.7	21	AAH62168	Phosphorylaes gly
8	21	0.7	21	AAH62169	Phosphorylaes gly
9	21	0.7	21	AAH62170	Phosphorylaes gly

10	21	0.7	21	AAH62171	Phosphorylaes gly
11	21	0.7	21	AAF97015	Human gene single
12	21	0.7	21	AAF97016	Human gene single
13	21	0.7	21	AAF97017	Human gene single
14	21	0.7	21	AAF97018	Human gene single
15	21	0.7	21	AAF97019	Human gene single
c 16	20	0.7	20	AA14008	Human liver glyco
c 17	20	0.7	20	AA14009	Human liver glyco
c 18	20	0.7	20	AA14010	Human liver glyco
c 19	20	0.7	20	AA14011	Human liver glyco
c 20	20	0.7	20	AA14012	Human liver glyco
c 21	20	0.7	20	AA14013	Human liver glyco
c 22	20	0.7	20	AA14014	Human liver glyco
c 23	20	0.7	20	AA14015	Human liver glyco
c 24	20	0.7	20	AA14016	Human liver glyco
c 25	20	0.7	20	AA14017	Human liver glyco
c 26	20	0.7	20	AA14018	Human liver glyco
c 27	20	0.7	20	AA14019	Human liver glyco
c 28	20	0.7	20	AA14020	Human liver glyco
c 29	20	0.7	20	AA14021	Human liver glyco
c 30	20	0.7	20	AA14022	Human liver glyco
c 31	20	0.7	20	AA14023	Human liver glyco
c 32	20	0.7	20	AA14024	Human liver glyco
c 33	20	0.7	20	AA14025	Human liver glyco
c 34	20	0.7	20	AA14026	Human liver glyco
c 35	20	0.7	20	AA14027	Human liver glyco
c 36	20	0.7	20	AA14028	Human liver glyco
c 37	20	0.7	20	AA14029	Human liver glyco
c 38	20	0.7	20	AA14030	Human liver glyco
c 39	20	0.7	20	AA14031	Human liver glyco
c 40	20	0.7	20	AA14032	Human liver glyco
c 41	20	0.7	20	AA14033	Human liver glyco
c 42	20	0.7	20	AA14034	Human liver glyco
c 43	20	0.7	20	AA14035	Human liver glyco
c 44	20	0.7	20	AA14036	Human liver glyco
c 45	20	0.7	20	AA14037	Human liver glyco

ALIGNMENTS

RESULT 1

AA14004

ID AA14004 standard; DNA; 27 BP.

AC AA14004;

XX 18-JUL-2000 (first entry)

DT Human liver glycogen phosphorylase quantitative real-time PCR probe #4.

XX Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;

DE 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGUPA;

KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;

KW expression inhibition; antisense therapy; hypoglycaemic;

KW type II diabetes; non insulin-dependent;

KW quantitative real-time PCR probe; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FF modified_base 1

FT /*tag= a

FT /note= "Conjugated to fluorescent reporter dye FAM"

FT modified_base 27

FT /*tag= b

FT /note= "Conjugated to fluorescent quencher dye TAMRA"

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

US6043091-A.

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XX PR 19-JUL-1999; 99US-0357071.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Cowser LM;
XX DR WPI; 2000-270346/23.
XX
XX Antisense compounds particularly oligonucleotides useful for
PT prophylaxis, diagnosis and treatment of diseases associated with
PT expression of liver glycogen phosphorylase
XX
XX Example 13; Column 38; 33pp; English.
XX
XX This sequence represents a human liver glycogen phosphorylase probe
CC used in quantitative real-time PCR with primers AAA14002-AL14003 in an
CC exemplification of the present invention. The invention relates to
CC antisense oligonucleotides targetted to the human liver glycogen
CC phosphorylase gene (PYGL gene), which inhibit its expression. A series
CC of oligonucleotides (AAA14008-AL14047) were designed to target different
CC regions of human liver glycogen phosphorylase RNA, and were analysed for
CC their effect on liver glycogen phosphorylase levels by quantitative
CC real-time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were
CC measured as a control. Liver glycogen phosphorylase is one of three
CC glycogen phosphorylase isozymes, which differ in their tissue-specific
CC distribution, immunological properties and electrophoretic mobilities
CC and are encoded by three different genes. Liver glycogen phosphorylase
CC is encoded by the PYGL gene, which is located on chromosome 14. Liver
CC glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate
CC alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active
CC form) catalyses the degradation of stored glycogen in the liver to
CC glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds.
CC It therefore plays a critical role in carbohydrate metabolism and blood
CC glucose homeostasis. Inhibition of liver glycogen phosphorylase and
CC therefore glycogenolysis may provide a means of reducing blood glucose
CC levels in diabetic patients, particularly those with type II (non
CC insulin-dependent) diabetes. The antisense oligonucleotides
CC of the invention are useful for diagnosis, prevention and treatment of
CC conditions associated with liver glycogen phosphorylase expression, or
CC those which may benefit from inhibition of liver glycogen phosphorylase
CC expression, such as type II diabetes.
XX
XX Sequence 27 BP; 5 A; 6 C; 8 G; 8 T; 0 other;
SQ
Query Match 1.0%; Score 27; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 437 ctgtgatgaggccattaccagcttgg 463
DB 1 ctgtgatgaggccattaccagcttgg 27
RESULT 2
AAA14002
ID AAA14002 standard; DNA; 21 BP.
XX AC AAA14002;
XX
XX 18-JUL-2000 (first entry)
XX Human liver glycogen phosphorylase quantitative real-time PCR primer #2.
XX Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;
KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;
KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;
KW expression inhibition; antisense therapy; hypoglycaemic;
KW type II diabetes; non insulin-dependent;
KW quantitative real-time PCR primer; ss.
XX Homo sapiens.
OS
```

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XX US6043091-A.
XX 28-MAR-2000.
XX
XX 19-JUL-1999; 99US-0357071.
XX 19-JUL-1999; 99US-0357071.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Cowser LM;
XX WPI; 2000-270346/23.
XX
XX Antisense compounds particularly oligonucleotides useful for
PT prophylaxis, diagnosis and treatment of diseases associated with
PT expression of liver glycogen phosphorylase
XX
XX Example 13; Column 38; 33pp; English.
XX
XX Sequences AAA14002-AL14003 represent human liver glycogen phosphorylase
CC PCR primers used in quantitative real-time PCR with probe AAA14003 in an
CC exemplification of the present invention. The invention relates to
CC antisense oligonucleotides targetted to the human liver glycogen
CC phosphorylase gene (PYGL gene), which inhibit its expression. A series
CC of oligonucleotides (AAA14008-AL14047) were designed to target different
CC regions of human liver glycogen phosphorylase RNA, and were analysed for
CC their effect on liver glycogen phosphorylase levels by quantitative
CC real-time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were
CC measured as a control. Liver glycogen phosphorylase is one of three
CC glycogen phosphorylase isozymes, which differ in their tissue-specific
CC distribution, immunological properties and electrophoretic mobilities
CC and are encoded by three different genes. Liver glycogen phosphorylase
CC is encoded by the PYGL gene, which is located on chromosome 14. Liver
CC glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate
CC alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active
CC form) catalyses the degradation of stored glycogen in the liver to
CC glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds.
CC It therefore plays a critical role in carbohydrate metabolism and blood
CC glucose homeostasis. Inhibition of liver glycogen phosphorylase and
CC therefore glycogenolysis may provide a means of reducing blood glucose
CC levels in diabetic patients, particularly those with type II (non
CC insulin-dependent) diabetes. The antisense oligonucleotides
CC of the invention are useful for diagnosis, prevention and treatment of
CC conditions associated with liver glycogen phosphorylase expression, or
CC those which may benefit from inhibition of liver glycogen phosphorylase
CC expression, such as type II diabetes.
XX
XX Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 other;
SQ
Query Match 0.7%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 386 catgggcccgaacattacagaa 406
DB 1 catgggcccgaacattacagaa 21
RESULT 3
AAA14003/C
ID AAA14003 standard; DNA; 21 BP.
XX AC AAA14003;
XX
XX 18-JUL-2000 (first entry)
XX Human liver glycogen phosphorylase quantitative real-time PCR primer #3.
XX Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;
KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;
```

glycogenolysis; carbohydrate metabolism; blood glucose homeostasis; expression inhibition; antisense therapy; hypoglycaemic; type II diabetes; non insulin-dependent; quantitative real-time PCR primer; ss.

Homo sapiens.

US6043091-A.

28-MAR-2000.

19-JUL-1999; 99US-0357071.

19-JUL-1999; 99US-0357071.

(ISIS-) ISIS PHARM INC.

Monia BP, Cowsett LM;

WPI; 2000-270346/23.

Antisense compounds particularly oligonucleotides useful for prophylaxis, diagnosis and treatment of diseases associated with expression of liver glycogen phosphorylase -

Example 13; Column 38; 33pp; English.

Sequences AAA14002-A14003 represent human liver glycogen phosphorylase PCR primers used in quantitative real-time PCR with probe AAA14003 in an exemplification of the present invention. The invention relates to antisense oligonucleotides targetted to the human liver glycogen phosphorylase gene (PYGL gene), which inhibit its expression. A series of oligonucleotides (AAA14008-A14047) were designed to target different regions of human liver glycogen phosphorylase RNA, and were analysed for their effect on liver glycogen phosphorylase levels by quantitative real-time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as a control. Liver glycogen phosphorylase is one of three glycogen phosphorylase isozymes, which differ in their tissue-specific distribution, immunological properties and electrophoretic mobilities and are encoded by three different genes. Liver glycogen phosphorylase is encoded by the PYGL gene, which is located on chromosome 14. Liver glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate form) catalyses the degradation of stored glycogen in the liver to glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds. It therefore plays a critical role in carbohydrate metabolism and blood glucose homeostasis. Inhibition of liver glycogen phosphorylase and therefore glycogenolysis may provide a means of reducing blood glucose levels in diabetic patients, particularly those with type II (non insulin-dependent) diabetes. The antisense oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with liver glycogen phosphorylase expression, or those which may benefit from inhibition of liver glycogen phosphorylase expression, such as type II diabetes.

Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 other;

Query Match 0.7%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 gacttggaatggtggtcttg 525
|||||

Db 21 GACTTGGAATGGTGTCTTG 1

RESULT 4
AAH62165
ID AAH62165 standard; DNA; 21 BP.
XX
AC AAH62165;
XX

12-SEP-2001 (first entry)
Phosphorylaes glycogen polymorphism containing DNA fragment #66.
Single nucleotide polymorphism; SNP; human; cancer; inflammation; heart disease; paternity testing; forensic science; ds.
Homo sapiens.
Key Location/Qualifiers
Variation replace(11,G)
/*tag= a
/standard_name= "single nucleotide polymorphism"
WO200138576-A2.
31-MAY-2001.
17-NOV-2000; 2000WO-US31639.
24-NOV-1999; 99US-0167334.
(WHED) WHITEHEAD INST BIOMEDICAL RES.
Cargill M, Ireland JS, Lander ES;
WPI; 2001-367705/38.
New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis -
Claim 1; Page 34; 80pp; English.
DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis.
Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1218 aaccagaagacctgcctac 1238
|||||

Db 1 aaccagaagacctgcctac 21

RESULT 5
AAH62166
ID AAH62166 standard; DNA; 21 BP.
XX
AC AAH62166;
XX
12-SEP-2001 (first entry)
Phosphorylaes glycogen polymorphism containing DNA fragment #67.
Single nucleotide polymorphism; SNP; human; cancer; inflammation; heart disease; paternity testing; forensic science; ds.
Homo sapiens.

PI Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-367705/38.

XX New nucleic acid segments of the human genome, particularly from genes
 XX including polymorphic sites, for phenotype correlation, forensics,
 PT paternity testing, medicine and genetic analysis -

XX Claim 1; Page 35; 80pp; English.

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
 CC contain single nucleotide polymorphisms (SNPs). A method is included in
 CC the invention for analysing a nucleic acid sample, which consists of
 CC determining the base occupying any one of the polymorphic sites given in
 CC the SNP containing sequences. The nucleotide sequences can be used in the
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
 CC diseases, diseases of the cardiovascular system, and infection by
 CC microorganisms. The oligonucleotides are also useful in the manufacture
 CC of a medicament for the treatment or prophylaxis of the diseases, and as
 CC a pharmaceutical. SNP containing oligonucleotides are useful in
 CC applications such as phenotype correlation, forensics, paternity testing,
 CC medicine and genetic analysis.

XX Sequence 21 BP; 4 A; 8 C; 7 G; 2 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.6e+04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 ctgcagcaccgaagcctcgg 2139

|||||

.Db 1 ctgcagcaccgaagcctcgg 21

RESULT 8

AAH62169

ID AAH62169 standard; DNA; 21 BP.

XX AC AAH62169;

XX 12-SEP-2001 (first entry)

XX Phosphorylaes glycogen polymorphism containing DNA fragment #70.

XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
 KW heart disease; paternity testing; forensic science; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Variation replace(11,A)

XX /*tag= a

XX /standard_name= "single nucleotide polymorphism"

XX WO200138576-A2.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-US31639.

XX 24-NOV-1999; 99US-0167334.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-367705/38.

XX New nucleic acid segments of the human genome, particularly from genes
 XX including polymorphic sites, for phenotype correlation, forensics,
 PT paternity testing, medicine and genetic analysis -

XX

PS Claim 1; Page 35; 80pp; English.

XX

CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which
 CC contain single nucleotide polymorphisms (SNPs). A method is included in
 CC the invention for analysing a nucleic acid sample, which consists of
 CC determining the base occupying any one of the polymorphic sites given in
 CC the SNP containing sequences. The nucleotide sequences can be used in the
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
 CC diseases, diseases of the cardiovascular system, and infection by
 CC microorganisms. The oligonucleotides are also useful in the manufacture
 CC of a medicament for the treatment or prophylaxis of the diseases, and as
 CC a pharmaceutical. SNP containing oligonucleotides are useful in
 CC applications such as phenotype correlation, forensics, paternity testing,
 CC medicine and genetic analysis.

XX Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.6e+04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2269 tggctgctttggacaagaag 2289

|||||

.Db 1 tggctgctttggacaagaag 21

RESULT 9

AAH62170

ID AAH62170 standard; DNA; 21 BP.

XX AC AAH62170;

XX 12-SEP-2001 (first entry)

XX Phosphorylaes glycogen polymorphism containing DNA fragment #71.

XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
 KW heart disease; paternity testing; forensic science; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Variation replace(11,A)

XX /*tag= a

XX /standard_name= "single nucleotide polymorphism"

XX WO200138576-A2.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-US31639.

XX 24-NOV-1999; 99US-0167334.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-367705/38.

XX New nucleic acid segments of the human genome, particularly from genes
 XX including polymorphic sites, for phenotype correlation, forensics,
 PT paternity testing, medicine and genetic analysis -

XX Claim 1; Page 35; 80pp; English.

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
 CC contain single nucleotide polymorphisms (SNPs). A method is included in
 CC the invention for analysing a nucleic acid sample, which consists of
 CC determining the base occupying any one of the polymorphic sites given in
 CC the SNP containing sequences. The nucleotide sequences can be used in the
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart

CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC a pharmaceutical. SNP containing oligonucleotides are useful in
CC applications such as phenotype correlation, forensics, paternity testing,
CC medicine and genetic analysis.

XX Sequence 21 BP; 8 A; 3 C; 9 G; 1 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2279 ggacaagaaagggtacgagcc 2299
|||||
Db 1 ggacaagaaagggtacgagcc 21

RESULT 10
AAH62171
ID AAH62171 standard; DNA; 21 BP.
AC AAH62171;
XX 12-SEP-2001 (first entry)
XX Phosphorylaes glycoen polymorphism containing DNA fragment #72.

XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW heart disease; paternity testing; forensic science; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Variation replace(11,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

XX WO200138576-A2.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-US31639.

XX 24-NOV-1999; 99US-0167334.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-367705/38.

XX New nucleic acid segments of the human genome, particularly from genes
PT including polymorphic sites, for phenotype correlation, forensics,
PT paternity testing, medicine and genetic analysis

XX Claim 1; Page 35; 80pp; English.

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC contain single nucleotide polymorphisms (SNPs). A method is included in
CC the invention for analysing a nucleic acid sample, which consists of
CC determining the base occupying any one of the polymorphic sites given in
CC the SNP containing sequences. The nucleotide sequences can be used in the
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC applications such as SNP containing oligonucleotides are useful in
CC medicine and genetic analysis.

XX Sequence 21 BP; 3 A; 4 C; 3 G; 11 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2350 ttgacaatggctttttctc 2370
|||||
Db 1 ttgacaatggctttttctc 21

RESULT 11
AAF97015
ID AAF97015 standard; DNA; 21 BP.

XX AAF97015;

XX 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #1776.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Variation replace(11,C)

FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

XX WO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000WO-US24503.

XX 10-SEP-1999; 99US-0153357.

XX 26-JUL-2000; 2000US-0220947.

XX 16-AUG-2000; 2000US-0225724.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis

XX Examples; Page 166; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification.

XX Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;

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Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1123 agctgaatgatactacaccc 1143
Db 1 agctgaatgatactacaccc 21

RESULT 12
AAF97016
ID AAF97016 standard; DNA; 21 BP.
XX AC AAF97016;
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #1777.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(11,C)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200118250-A2.
XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US24503.
XX PR 10-SEP-1999; 99US-0153357.
XX PR 26-JUL-2000; 2000US-0220947.
XX PR 16-AUG-2000; 2000US-0225724.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI: 2001-226749/23.
XX DR Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis -
XX PS Examples; Page 166; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism
XX CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification.
XX SQ Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1873 tgtacaaccgcattagaagaag 1893
Db 1 tgtacaaccgcattagaagaag 21

Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1978 agctgatacttcagtgagcag 1998
Db 1 agctgatacttcagtgagcag 21

RESULT 13
AAF97017
ID AAF97017 standard; DNA; 21 BP.
XX AC AAF97017;
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #1778.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(11,T)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200118250-A2.
XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US24503.
XX PR 10-SEP-1999; 99US-0153357.
XX PR 26-JUL-2000; 2000US-0220947.
XX PR 16-AUG-2000; 2000US-0225724.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI: 2001-226749/23.
XX DR Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis -
XX PS Examples; Page 166; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism
XX CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification.
XX SQ Sequence 21 BP; 9 A; 4 C; 4 G; 4 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1873 tgtacaaccgcattagaagaag 1893
Db 1 tgtacaaccgcattagaagaag 21

```

```
RESULT 14
AAF97018
ID AAF97018 standard; DNA; 21 BP.
XX
AC AAF97018;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1779.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,G)
FT FT /*tag= a
FT FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US24503.
XX
PR 10-SEP-1999; 99US-0153357.
PR 26-JUL-2000; 2000US-0220947.
PR 16-AUG-2000; 2000US-0225724.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis -
XX
PS Examples; Page 166; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification.
XX
SQ Sequence 21 BP; 8 A; 3 C; 4 G; 6 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2027 aagcaagttgaaagtcattc 2047
Db 1 aagcaagttgaaagtcattc 21

RESULT 15
```

```
AAF97019
ID AAF97019 standard; DNA; 21 BP.
XX
AC AAF97019;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1780.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,G)
FT FT /*tag= a
FT FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US24503.
XX
PR 10-SEP-1999; 99US-0153357.
PR 26-JUL-2000; 2000US-0220947.
PR 16-AUG-2000; 2000US-0225724.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis -
XX
PS Examples; Page 166; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification.
XX
SQ Sequence 21 BP; 5 A; 4 C; 8 G; 4 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 gatgtggaccctctgagaagg 1397
Db 1 gatgtggaccctctgagaagg 21

Search completed: September 7, 2002, 02:10:17
Job time: 6483 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 23:49:24 ; Search time 65.96 Seconds
(without alignments)
10531.406 Million cell updates/sec

Title: US-10-019-470-1

Perfect score: 2828

Sequence: 1 gttgaagctcctgcgcgg.....aaagtgtcaattccaagga 2828

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 403436

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:**

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:**

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	1.0	27	US-09-357-071-4	Sequence 4, Appli
2	21	0.7	21	US-09-357-071-2	Sequence 2, Appli
3	21	0.7	21	US-09-357-071-3	Sequence 3, Appli
4	20	0.7	20	US-09-357-071-8	Sequence 8, Appli
5	20	0.7	20	US-09-357-071-9	Sequence 9, Appli
6	20	0.7	20	US-09-357-071-10	Sequence 10, Appli
7	20	0.7	20	US-09-357-071-11	Sequence 11, Appli
8	20	0.7	20	US-09-357-071-12	Sequence 12, Appli
9	20	0.7	20	US-09-357-071-13	Sequence 13, Appli
10	20	0.7	20	US-09-357-071-14	Sequence 14, Appli
11	20	0.7	20	US-09-357-071-15	Sequence 15, Appli
12	20	0.7	20	US-09-357-071-16	Sequence 16, Appli
13	20	0.7	20	US-09-357-071-17	Sequence 17, Appli
14	20	0.7	20	US-09-357-071-18	Sequence 18, Appli
15	20	0.7	20	US-09-357-071-19	Sequence 19, Appli
16	20	0.7	20	US-09-357-071-20	Sequence 20, Appli
17	20	0.7	20	US-09-357-071-21	Sequence 21, Appli
18	20	0.7	20	US-09-357-071-22	Sequence 22, Appli
19	20	0.7	20	US-09-357-071-23	Sequence 23, Appli
20	20	0.7	20	US-09-357-071-24	Sequence 24, Appli
21	20	0.7	20	US-09-357-071-25	Sequence 25, Appli
22	20	0.7	20	US-09-357-071-26	Sequence 26, Appli
23	20	0.7	20	US-09-357-071-27	Sequence 27, Appli
24	20	0.7	20	US-09-357-071-28	Sequence 28, Appli
25	20	0.7	20	US-09-357-071-29	Sequence 29, Appli
26	20	0.7	20	US-09-357-071-30	Sequence 30, Appli
27	20	0.7	20	US-09-357-071-31	Sequence 31, Appli

ALIGNMENTS

RESULT 1

US-09-357-071-4
; Sequence 4, Application US/09357071
; Patent No. 6043091

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowser

TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSIO

FILE REFERENCE: RTS-0074

CURRENT APPLICATION NUMBER: US/09/357,071

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 4

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: PCR Probe

US-09-357-071-4

Query Match 1.0%; Score 27; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 ctgtgatgagccattaccagcttgg 463

Db 1 ctgtgatgagccattaccagcttgg 27

RESULT 2

US-09-357-071-2

; Sequence 2, Application US/09357071

; Patent No. 6043091

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowser

TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSIO

FILE REFERENCE: RTS-0074

CURRENT APPLICATION NUMBER: US/09/357,071

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 2

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: PCR Primer

US-09-357-071-2

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Query Match          0.7%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 catggccgaacattacagaa 406
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Db 1 catggccgaacattacagaa 21

RESULT 3
US-09-357-071-3/c
; Sequence 3, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-357-071-3

Query Match          0.7%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 gacttggcaatggtgtctt 525
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Db 21 GACTTGGCAATGCTGTCTT 1

RESULT 4
US-09-357-071-8/c
; Sequence 8, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-8

Query Match          0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ctctggcgcgcggcg 28
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Db 20 CTCTGGCGCGCGGCGG 1

RESULT 5
US-09-357-071-9/c
; Sequence 9, Application US/09357071
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; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-9
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Query Match          0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 71 ccagctctctcgcagccg 90
|||||
Db 20 CCAGCTCTCTCGCAGCCG 1
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```
RESULT 6
US-09-357-071-10/c
; Sequence 10, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-10
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Query Match          0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 109 cagccatggcggaaccgctg 128
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Db 20 CAGCCATGGCGGAACCGCTG 1
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RESULT 7
US-09-357-071-11/c
; Sequence 11, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-11

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 atggcggaaccgctgacaga 133
|||||
Db 20 ATGGCGGAACCGCTGACAGA 1

RESULT 8

US-09-357-071-12/c
; Sequence 12, Application US/09357071
; Patent No. 6043091

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION

; FILE REFERENCE: RTS-0074

; CURRENT APPLICATION NUMBER: US/09/357,071

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 12

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-357-071-12

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 tggcgctggagaaactgcca 191
|||||
Db 20 TGGCGCTGGAGAACGTGCCA 1

RESULT 9

US-09-357-071-13/c
; Sequence 13, Application US/09357071
; Patent No. 6043091

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION

; FILE REFERENCE: RTS-0074

; CURRENT APPLICATION NUMBER: US/09/357,071

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 13

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-357-071-13

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 tgcacttcacgctggtcaag 239
|||||
Db 20 TGCACCTTACGCTGGTCAAG 1

RESULT 10

US-09-357-071-14/c
; Sequence 14, Application US/09357071
; Patent No. 6043091

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION

; FILE REFERENCE: RTS-0074

; CURRENT APPLICATION NUMBER: US/09/357,071

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 14

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-357-071-14

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 ccgcgactactacttcgcgc 279
|||||
Db 20 CCGCGACTACTACTTCGCGC 1

RESULT 11

US-09-357-071-15/c
; Sequence 15, Application US/09357071
; Patent No. 6043091

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION

; FILE REFERENCE: RTS-0074

; CURRENT APPLICATION NUMBER: US/09/357,071

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 15

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-357-071-15

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 ccacctgtggcgctgga 318
|||||
Db 20 CCACCTGTGGGGCGCTGGA 1

RESULT 12

US-09-357-071-16/c
; Sequence 16, Application US/09357071
; Patent No. 6043091

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION

; FILE REFERENCE: RTS-0074

; CURRENT APPLICATION NUMBER: US/09/357,071

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-16

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 tctctggaattttacatggg 391
Db 20 TCTCTGGAATTTACATGG 1

RESULT 13
US-09-357-071-17/c
; Sequence 17, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-17

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Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 tcaacctcggtctgcaaaat 434
Db 20 TCAACCTCGGTCTGCAAAAT 1

RESULT 14
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; Sequence 18, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-18

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 ttggattggatatagaagag 479
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RESULT 15
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; Sequence 19, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-19

Query Match 0.7%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 ttggagagacttgctgctgc 542
Db 20 TTGGGAGACTTGCTGCTGC 1

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GenCore version 4.5
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OM nucleic -- nucleic search, using sw model

Run on: September 7, 2002, 00:29:44 ; Search time 3515.76 Seconds
(without alignments)
17402.637 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	21	0.7	21	1	PCT-US00-19019-3
5	21	0.7	21	37	US-10-019-470-2
c 6	21	0.7	21	37	US-10-019-470-3
7	20.6	0.7	21	25	US-09-657-472-1780
8	20.6	0.7	21	25	US-09-657-472-1781
9	20.6	0.7	21	25	US-09-657-472-1782
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11	20.6	0.7	21	25	US-09-657-472-1784
12	20.6	0.7	21	28	US-09-715-849-66
13	20.6	0.7	21	28	US-09-715-849-67
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c 24	20	0.7	20	1	PCT-US00-19019-9
c 25	20	0.7	20	1	PCT-US00-19019-10
c 26	20	0.7	20	1	PCT-US00-19019-11
c 27	20	0.7	20	1	PCT-US00-19019-12
c 28	20	0.7	20	1	PCT-US00-19019-13
c 29	20	0.7	20	1	PCT-US00-19019-14
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c 31	20	0.7	20	1	PCT-US00-19019-16
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					Sequence 1782, Ap
					Sequence 1783, Ap
					Sequence 1784, Ap
					Sequence 66, Appl
					Sequence 67, Appl
					Sequence 68, Appl
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					Sequence 70, Appl
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					Sequence 571131,
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					Sequence 15, Appl
					Sequence 16, Appl

Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
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ALIGNMENTS

RESULT 1
PCT-US00-19019-4
; Sequence 4, Application PC/TUS0019019
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: ISIS PHARMACEUTICALS, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTSP-0056
; CURRENT APPLICATION NUMBER: PCT/US00/19019
; CURRENT FILING DATE: 2000-07-12
; EARLIER FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
PCT-US00-19019-4

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 ctgtgatgagccattaccagcttg 463
Db 1 ctgtgatgagccattaccagcttg 27

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US-10-019-470-4
; Sequence 4, Application US/10019470
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/019,470
; CURRENT FILING DATE: 2001-12-28
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-019-470-4

Query Match 1.0%; Score 27; DB 37; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 ctgtgatgagccattaccagcttg 463
Db 1 ctgtgatgagccattaccagcttg 27

RESULT 3
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; Sequence 2, Application PC/TUS0019019
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: ISIS PHARMACEUTICALS, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTSP-0056
; CURRENT APPLICATION NUMBER: PCT/US00/19019
; CURRENT FILING DATE: 2000-07-12
; EARLIER FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
PCT-US00-19019-2

Query Match 0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 catgggcccgaacattacagaa 406
Db 1 catgggcccgaacattacagaa 21

RESULT 4
PCT-US00-19019-3/c
; Sequence 3, Application PC/TUS0019019
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: ISIS PHARMACEUTICALS, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTSP-0056
; CURRENT APPLICATION NUMBER: PCT/US00/19019
; CURRENT FILING DATE: 2000-07-12
; EARLIER FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
PCT-US00-19019-3

Query Match 0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 gacttgccaatggtgcttg 525
Db 21 GACTTGCCAATGGTGCTTG 1

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RESULT 5
US-10-019-470-2
; Sequence 2, Application US/10019470
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/019,470
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-019-470-2

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Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 catggccgcgaacattacagaa 406
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Db 1 catggccgcgaacattacagaa 21

RESULT 6
US-10-019-470-3/c
; Sequence 3, Application US/10019470
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/019,470
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-019-470-3

Query Match          0.7%; Score 21; DB 37; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 gacttggcaatgggtcttg 525
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Db 21 GACTTGGCAATGGGTCTTG 1

RESULT 7
US-09-657-472-1780
; Sequence 1780, Application US/09657472
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

Query Match          0.7%; Score 21; DB 37; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 gacttggcaatgggtcttg 525
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Db 21 GACTTGGCAATGGGTCTTG 1

RESULT 8
US-09-657-472-1781
; Sequence 1781, Application US/09657472
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1781
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1781

Query Match          0.7%; Score 20.6; DB 25; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1123 agctgaatgatactcacctc 1143
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Db 1 agctgaatgatactcacctc 21

RESULT 9
US-09-657-472-1782
; Sequence 1782, Application US/09657472
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

Query Match          0.7%; Score 20.6; DB 25; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1978 agctgatacttcagtggcag 1998
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Db 1 agctgatacttcagtggcag 21
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; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1782
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1782
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Query Match 0.7%; Score 20.6; DB 25; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 1 tgtacaaccgcattagaagaag 21
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RESULT 10
US-09-657-472-1783
; Sequence 1783, Application US/09657472
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1783
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1783
```

```
Query Match 0.7%; Score 20.6; DB 25; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2027 aagcaagttgaaagtcatctt 2047
|||||:|||||:|||||:
Db 1 aagcaagttgaaagtcatctt 21
```

```
RESULT 11
US-09-657-472-1784
; Sequence 1784, Application US/09657472
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
```

```
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1784
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1784
```

```
Query Match 0.7%; Score 20.6; DB 25; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1377 gatgtggaccctctgagaagg 1397
|||||:|||||:|||||:
Db 1 gatgtggaccctctgagaagg 21
```

```
RESULT 12
US-09-715-849-66
; Sequence 66, Application US/09715849
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2002-001
; CURRENT APPLICATION NUMBER: US/09/715,849
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/167,334
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-715-849-66
```

```
Query Match 0.7%; Score 20.6; DB 28; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1218 aaccagaagaccttcgacctac 1238
|||||:|||||:|||||:
Db 1 aaccagaagaccttcgacctac 21
```

```
RESULT 13
US-09-715-849-67
; Sequence 67, Application US/09715849
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2002-001
```

; CURRENT APPLICATION NUMBER: US/09/715,849
 ; CURRENT FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: US 60/167,334
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 67
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-715-849-67

Query Match 0.7%; Score 20.6; DB 28; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.4e+06;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1706 cctcgggaactcgccaaggt 1726
 Db 1 cctcgggaactcgccaaggt 21

RESULT 14

US-09-715-849-68
 ; Sequence 68, Application US/09715849
 ; GENERAL INFORMATION:
 ; APPLICANT: Cargill, Michele
 ; APPLICANT: Ireland, James S.
 ; APPLICANT: Lander, Eric S.
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: 2825.2002-001
 ; CURRENT APPLICATION NUMBER: US/09/715,849
 ; CURRENT FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: US 60/167,334
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 68
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-715-849-68

Query Match 0.7%; Score 20.6; DB 28; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.4e+06;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2003 ggtgaacaatgacctatggt 2023
 Db 1 ggtgaacaatgacctatggt 21

RESULT 15

US-09-715-849-69
 ; Sequence 69, Application US/09715849
 ; GENERAL INFORMATION:
 ; APPLICANT: Cargill, Michele
 ; APPLICANT: Ireland, James S.
 ; APPLICANT: Lander, Eric S.
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: 2825.2002-001
 ; CURRENT APPLICATION NUMBER: US/09/715,849
 ; CURRENT FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: US 60/167,334
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 69
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-715-849-69

Query Match 0.7%; Score 20.6; DB 28; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.4e+06;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2119 ctgcaggcaccgagcctcgg 2139
 Db 1 ctgcaggcaccgagcctcgg 21

Search completed: September 7, 2002, 03:09:15
 Job time: 9571 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 01:05:04 ; Search time 495.36 Seconds
(without alignments)
17386.191 Million cell updates/sec

Title: US-10-019-470-1

Perfect score: 2828

Sequence: 1 gttgaagctctgcggcgg.....aaagtgtcaatttccaagga 2828

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2036664 seqs, 1522705736 residues

Total number of hits satisfying chosen parameters: 888728

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	27	1.0	27	7 US-10-114-544-4	Sequence 4, Appli
2	21	0.7	21	7 US-10-114-544-2	Sequence 2, Appli
3	21	0.7	21	7 US-10-114-544-3	Sequence 3, Appli
4	20	0.7	20	7 US-10-114-544-8	Sequence 8, Appli
5	20	0.7	20	7 US-10-114-544-9	Sequence 9, Appli
6	20	0.7	20	7 US-10-114-544-10	Sequence 10, Appli
7	20	0.7	20	7 US-10-114-544-11	Sequence 11, Appli
8	20	0.7	20	7 US-10-114-544-12	Sequence 12, Appli
9	20	0.7	20	7 US-10-114-544-13	Sequence 13, Appli
10	20	0.7	20	7 US-10-114-544-14	Sequence 14, Appli
11	20	0.7	20	7 US-10-114-544-15	Sequence 15, Appli
12	20	0.7	20	7 US-10-114-544-16	Sequence 16, Appli
13	20	0.7	20	7 US-10-114-544-17	Sequence 17, Appli
14	20	0.7	20	7 US-10-114-544-18	Sequence 18, Appli
15	20	0.7	20	7 US-10-114-544-19	Sequence 19, Appli
16	20	0.7	20	7 US-10-114-544-20	Sequence 20, Appli
17	20	0.7	20	7 US-10-114-544-21	Sequence 21, Appli
18	20	0.7	20	7 US-10-114-544-22	Sequence 22, Appli
19	20	0.7	20	7 US-10-114-544-23	Sequence 23, Appli
20	20	0.7	20	7 US-10-114-544-24	Sequence 24, Appli
21	20	0.7	20	7 US-10-114-544-25	Sequence 25, Appli
22	20	0.7	20	7 US-10-114-544-26	Sequence 26, Appli
23	20	0.7	20	7 US-10-114-544-27	Sequence 27, Appli
24	20	0.7	20	7 US-10-114-544-28	Sequence 28, Appli
25	20	0.7	20	7 US-10-114-544-29	Sequence 29, Appli

```

c 26 20 0.7 20 7 US-10-114-544-30 Sequence 30, Appli
c 27 20 0.7 20 7 US-10-114-544-31 Sequence 31, Appli
c 28 20 0.7 20 7 US-10-114-544-32 Sequence 32, Appli
c 29 20 0.7 20 7 US-10-114-544-33 Sequence 33, Appli
c 30 20 0.7 20 7 US-10-114-544-34 Sequence 34, Appli
c 31 20 0.7 20 7 US-10-114-544-35 Sequence 35, Appli
c 32 20 0.7 20 7 US-10-114-544-36 Sequence 36, Appli
c 33 20 0.7 20 7 US-10-114-544-37 Sequence 37, Appli
c 34 20 0.7 20 7 US-10-114-544-38 Sequence 38, Appli
c 35 20 0.7 20 7 US-10-114-544-39 Sequence 39, Appli
c 36 20 0.7 20 7 US-10-114-544-40 Sequence 40, Appli
c 37 20 0.7 20 7 US-10-114-544-41 Sequence 41, Appli
c 38 20 0.7 20 7 US-10-114-544-42 Sequence 42, Appli
c 39 20 0.7 20 7 US-10-114-544-43 Sequence 43, Appli
c 40 20 0.7 20 7 US-10-114-544-44 Sequence 44, Appli
c 41 20 0.7 20 7 US-10-114-544-45 Sequence 45, Appli
c 42 20 0.7 20 7 US-10-114-544-46 Sequence 46, Appli
c 43 20 0.7 20 7 US-10-114-544-47 Sequence 47, Appli
c 44 19.6 0.7 27 7 US-10-023-586B-5 Sequence 5, Appli
c 45 19.2 0.7 25 5 US-09-396-196G-97605 Sequence 97605, A

```

ALIGNMENTS

```

RESULT 1
US-10-114-544-4
; Sequence 4, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; PRIOR FILING DATE: 2002-04-01
; PRIOR FILING DATE: 2001-12-28
; PRIOR FILING DATE: 2001-12-28
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-114-544-4

```

```

Query Match 1.0%; Score 27; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 437 ctgtgatgagccattaccagcttgg 463
Db 1 ctgtgatgagccattaccagcttgg 27

```

```

RESULT 2
US-10-114-544-2
; Sequence 2, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; PRIOR FILING DATE: 2002-04-01
; PRIOR FILING DATE: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071

```

; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-2

Query Match 0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 catgggccaacattacagaa 406
Db 1 catgggccaacattacagaa 21

RESULT 3
US-10-114-544-3/c
; Sequence 3, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-3

Query Match 0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 gacttgccaatggtgctcttg 525
Db 21 GACTTGCAATGCTGCTTG 1

RESULT 4
US-10-114-544-8/c
; Sequence 8, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-8

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ctctctgctgctgctgctgctg 28
Db 20 CTCTGCTGCTGCTGCTGCTG 1

RESULT 5
US-10-114-544-9/c
; Sequence 9, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-9

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 ccagctctctgctgctgctgctg 90
Db 20 CCAGCTCTCTGCTGCTGCTGCTG 1

RESULT 6
US-10-114-544-10/c
; Sequence 10, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-10

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 cagccatggcgcaaccgctg 128
|||||
DB 20 CAGCCATGGCGCAACCGCTG 1

RESULT 7
US-10-114-544-11/c
; Sequence 11, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-11

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 atggcgcaaccgctgacaga 133
|||||
DB 20 ATGGCGCAACCGCTGACAGA 1

RESULT 8
US-10-114-544-12/c
; Sequence 12, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-12

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 tggcgctggagaacgtggca 191
|||||
DB 20 TGGCGCTGGAGAACGTGGCA 1

RESULT 9
US-10-114-544-13/c
; Sequence 13, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-13

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 tgcacttcacgctggctcaag 239
|||||
DB 20 TGCACCTTCACGCTGGCTCAAG 1

RESULT 10
US-10-114-544-14/c
; Sequence 14, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-14

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 ccgcgactactcttcgcgc 279
|||||
DB 20 CCGCGACTACTCTTCGCGC 1

RESULT 11
US-10-114-544-15/c
; Sequence 15, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-15

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 ccacctgtggggcgctgga 318
|||||
Db 20 CCACCTGGTGGGCGCTGGA 1

RESULT 12
US-10-114-544-16/c
; Sequence 16, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-16

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 tctctggaattttacatggg 391
|||||
Db 20 TCTCTGGAATTTTACATGGG 1

RESULT 13
US-10-114-544-17/c
; Sequence 17, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-17

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 tcaacctcggtctgcaaat 434
|||||
Db 20 TCAACCTCGGTCTGCAAAAT 1

RESULT 14
US-10-114-544-18/c
; Sequence 18, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-18

Query Match 0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 ttggattggatataagaag 479
|||||
Db 20 TTGGATTGGATATAGAAGAG 1

RESULT 15
US-10-114-544-19/c
; Sequence 19, Application US/10114544
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544

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; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-344-19
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Query Match      0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 523 ttgggagacttgctgcctgc 542
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Db 20 TTGGGAGACTTGCTGCCTGC 1
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Search completed: September 7, 2002, 03:17:51
Job time: 7967 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 23:29:44 ; Search time 2157 Seconds
(without alignments)
17695.591 Million cell updates/sec

Title: US-10-019-470-1
Perfect score: 2828
Sequence: 1 gttgaagctctgcgcgg.....aaagtgtcaattccaagga 2828

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 28088

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estb.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_gss.*
13: gb_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.2	0.6	28	12	AZ782046
2	17.2	0.6	29	12	AZ514403
3	16.6	0.6	30	12	AZ990068
4	16.4	0.6	29	12	AZ331559
5	16	0.6	26	10	D11539
6	16	0.6	27	12	TA128C06P
7	16	0.6	28	12	AZ760461
8	16	0.6	29	12	AZ323903
9	16	0.6	29	12	AZ658502
10	16	0.6	30	12	AZ458346
11	15.8	0.6	23	12	AZ433969
12	15.8	0.6	27	10	D25863
13	15.8	0.6	28	9	A1826975
14	15.8	0.6	28	12	AZ799395
15	15.8	0.6	29	12	AZ475726
16	15.8	0.6	30	10	T63438
17	15.8	0.6	30	12	AZ433900

c 18	15.6	0.6	25	12	TA232H10P	AL481055 T. brucei
c 19	15.6	0.6	26	12	AZ832213	AZ832213 2M0112C03
c 20	15.6	0.6	28	9	A1815651	A1815651 au49b06.y
c 21	15.6	0.6	28	12	AZ458545	AZ458545 1M0262B15
c 22	15.6	0.6	29	12	TA18B08P	AL451961 T. brucei
c 23	15.4	0.5	25	9	A1808531	A1808531 wf95e12.x
c 24	15.4	0.5	25	10	C21101	C21101 HUMGS000262
c 25	15.4	0.5	25	10	C21203	C21203 HUMGS000223
c 26	15.4	0.5	26	12	AZ579502	AZ579502 1M0367D12
c 27	15.4	0.5	28	12	AZ648296	AZ648296 1M0517E15
c 28	15.2	0.5	30	12	AZ475143	AZ475143 1M0293G22
c 29	15.2	0.5	28	9	AA027602	AA027602 ml12d08.r
c 30	15.2	0.5	28	9	A1687937	A1687937 tp99d01.x
c 31	15.2	0.5	28	12	AZ466667	AZ466667 1M0277G06
c 32	15.2	0.5	29	9	AU014027	AU014027 AU014027
c 33	15.2	0.5	29	12	AZ587944	AZ587944 1M0395O23
c 34	15.2	0.5	30	12	AZ421244	AZ421244 1M0199K20
c 35	15.2	0.5	30	12	TA158G08P	AL472082 T. brucei
c 36	15	0.5	24	12	AZ807245	AZ807245 2M0069W24
c 37	15	0.5	25	12	AZ485096	AZ485096 1M0311K10
c 38	15	0.5	25	12	AZ817944	AZ817944 2M0087M12
c 39	15	0.5	25	12	AZ831709	AZ831709 2M0111O06
c 40	15	0.5	26	12	TA175A08P	AL475157 T. brucei
c 41	15	0.5	26	12	TA215H05P	AL479558 T. brucei
c 42	15	0.5	28	12	AZ784264	AZ784264 2M0026I20
c 43	15	0.5	30	12	AZ400595	AZ400595 1M0166P19
c 44	15	0.5	30	12	AZ658957	AZ658957 1M0536H04
c 45	14.8	0.5	23	12	AZ973344	AZ973344 2M0247H06

ALIGNMENTS

RESULT 1
AZ782046 28 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0021N19R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGC2M0021N19 R, DNA sequence.

ACCESSION AZ782046
VERSION AZ782046.1 GI:12915346

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0021 row: N column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0021N19"
/clone_lib="Mouse 10kb plasmid UUGCLM library"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
7 a 9 c 4 g 8 t
BASE COUNT
ORIGIN

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Query Match 0.6%; Score 17.2; DB 12; Length 28;
Best Local Similarity 86.4%; Pred. No. 7.8e+06;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1594 tactctgaaccaggacttgc 1615
||||| ||||||||| ||
Db 2 TACTCTTAACCCAGGACTGGC 23

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```

RESULT 2
A2514403/c
LOCUS
DEFINITION
29 bp DNA linear GSS 05-OCT-2000
clone UUGC1M0361K06 F, DNA sequence.

```

```

ACCESSION A2514403
VERSION A2514403.1 GI:10695719
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: K column: 06
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1..29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361K06"

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FEATURES
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1..29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361K06"

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
5 a 6 c 4 g 14 t
BASE COUNT
ORIGIN

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Query Match 0.6%; Score 17.2; DB 12; Length 29;
Best Local Similarity 86.4%; Pred. No. 7.9e+06;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 466 tggatataagaagagttagaaga 487
||||| ||||||||| || ||||
Db 29 TGAATATAGAAGAGATAAAGA 8

```

RESULT 3

```

A2990068
LOCUS
DEFINITION
30 bp DNA linear GSS 27-APR-2001
clone UUGC2M0273G07 R, DNA sequence.

```

```

ACCESSION A2990068
VERSION A2990068.1 GI:13861295
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: G column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1..30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

```

REFERENCE

```

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

```

TITLE

```

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

```

JOURNAL

```

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: G column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1..30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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FEATURES

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source
1..30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC2M0273G07"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      7 a  12 c  8 g  3 t
ORIGIN

```

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Query Match      0.6%; Score 16.6; DB 12; Length 30;
Best Local Similarity 82.6%; Pred. No. 1.1e+07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 241 accgcaacgtggccaccacccgc 263
      |||| ||||| ||| |||| |
Db 8 ACCGGAAGCTGGACACGACCCAC 30

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RESULT 4
LOCUS AZ331559/c 29 bp DNA linear GSS 29-SEP-2000
DEFINITION M0059L06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0059L06 R, DNA sequence.
ACCESSION AZ331559
VERSION AZ331559.1 GI:10394372
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: L column: 06
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
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Source Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"

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/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      3 a  7 c  8 g  11 t
ORIGIN

```

```

Query Match      0.6%; Score 16.4; DB 12; Length 29;
Best Local Similarity 76.9%; Pred. No. 1.2e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 726 ggaagaagtagaacacacacacccgg 751
      ||||| ||||| ||||| ||||| ||
Db 27 GGAATGATGAACACCCCCACACAGG 2

```

```

RESULT 5
LOCUS D11539 26 bp mRNA linear EST 21-JUL-1994
DEFINITION HUMC12B04 Liver HepG2 cell line. Homo sapiens cDNA clone ci2b04 3', mRNA sequence.
ACCESSION D11539
VERSION D11539.1 GI:511920
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y. and Matsubara,K.
TITLE Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression
JOURNAL Nature Genet. 2, 173-179 (1992)
COMMENT 94258199
Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES
Source Location/Qualifiers
1..26
/organism="Homo sapiens"
/db_xref="GDB:D08804IE"
/db_xref="taxon:9606"
/clone="ci2b04"
/clone_lib="Liver HepG2 cell line."
/lab_host="E.coli"
/notes="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."
BASE COUNT      12 a  2 c  5 g  7 t
ORIGIN

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Query Match 0.6%; Score 16; DB 10; Length 26;
 Best Local Similarity 79.2%; Pred. No. 1.5e+07;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2633 atctacaaagtcaatggaattg 2656
 ||| || ||||| ||| |||||
 Db 2 ATCAAGAAAGTTTATGAAATG 25

RESULT 6
 TA128C06P/c
 LOCUS T. brucei sheared genomic DNA clone 128c06, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL464342
 VERSION AL464342.1 GI:11834605
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei.
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genomic Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
 source
 1..27
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="128c06"
 5 a 3 c 8 g 11 t

BASE COUNT 5 a 3 c 8 g 11 t
 ORIGIN

Query Match 0.6%; Score 16; DB 12; Length 27;
 Best Local Similarity 79.2%; Pred. No. 1.5e+07;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 414 atcaactcggtcgcaaaatgcc 437
 ||| || ||||| ||| |||||
 Db 26 AACAACTTCGTTTGCAAAAGCC 3

RESULT 7
 AZ760461
 LOCUS AZ760461 28 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0554C13F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0554C13 F, DNA sequence.
 ACCESSION AZ760461
 VERSION AZ760461.1 GI:12868327
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENTFEATURES
source

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0554 row: C column: 13
 Seq primer: CGTTGTAAACGACGGCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

Location/Qualifiers

1..28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0554C13"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g1473211419b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-cold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 12 c 2 g 7 t
 ORIGIN

Query Match 0.6%; Score 16; DB 12; Length 28;
 Best Local Similarity 79.2%; Pred. No. 1.5e+07;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 258 acccgcgactactctgcgctg 281
 ||| || ||||| ||| |||||

Db 1 ACCTGCTACACTACTCTCTCTG 24

RESULT 8
 AZ323903/c
 LOCUS AZ323903 29 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0045A07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0045A07 R, DNA sequence.
 ACCESSION AZ323903
 VERSION AZ323903.1 GI:10379084
 KEYWORDS GSS.
 SOURCE house mouse.


```

ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: A column: 07
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0045A07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 9 a 5 c 10 g 5 t
ORIGIN
Query Match 0.6%; Score 16; DB 12; Length 29;
Best Local Similarity 79.2%; Pred. No. 1.5e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1067 ctccaccgtgtgtaagaaactgt 1090
||||| ||||| ||||| |||||
Db 24 CTTCCCGCGTGTCAATGACCTGT 1

RESULT 9
AZ658502 29 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION IM0535M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0535M12 F, DNA sequence.
ACCESSION AZ658502
VERSION AZ658502.1 GI:11795564
KEYWORDS GSS.

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0535 row: M column: 12
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0535M12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 7 a 5 c 9 g 8 t
ORIGIN
Query Match 0.6%; Score 16; DB 12; Length 29;
Best Local Similarity 79.2%; Pred. No. 1.5e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2224 ctggggaagagaacctgttcattc 2247
||||| ||||| ||||| |||||
Db 5 CAGGGGCAGAGAACTCTGCTGATCT 28

RESULT 10
AZ458346 30 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION IM0262p13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0262p13 F, DNA sequence.
ACCESSION AZ458346
VERSION AZ458346.1 GI:10616471

```

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: P column: 13

Seq primer: CTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 30.

FEATURES
source
1. 30
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0220E07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 7 a 4 c 10 g 9 t
ORIGIN

Query Match 0.6%; Score 16; DB 12; Length 30;
Best Local Similarity 79.2%; Pred. No. 1.6e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2448 gaagcctatgtcaagtgtcaagat 2471
||||| ||||| ||||| |||||

Db 6 GAAGTCTCTGTCAGGTGTGATGAT 29

RESULT 11
AZ433969/c 23 bp DNA linear GSS 03-OCT-2000

LOCUS 1M0220E07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0220E07 F, DNA sequence.

ACCESSION AZ433969

AZ433969.1 GI:10557982
GSS.
house mouse.

Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: E column: 07

Seq primer: CTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source
1. 23
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0220E07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 5 a 3 c 4 g 11 t
ORIGIN

Query Match 0.6%; Score 15.8; DB 12;
Best Local Similarity 89.5%; Pred. No. 1.5e+07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1553 tcagaataaaacccaatggg 1571
||||| ||||| ||||| |||||

Db 23 TCAGAAAAAACCAATGTG 5

RESULT 12
D25863 27 bp mRNA linear EST 30-NOV-1995

LOCUS HUMGS04241 Human colon mucosa Homo sapiens cDNA clone cm1743 3',
DEFINITION mRNA sequence.

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ACCESSION      D25863.1  GI:500531
VERSION        D25863.1
KEYWORDS       EST.
SOURCE         Homo sapiens
ORGANISM       Human.

REFERENCE
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE         Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL       1 (bases 1 to 27)
COMMENT       Global analysis of gene expression in colon mucosa: a large scale
              random cDNA sequencing analysis
              Unpublished (1994)
              Contact: Okubo,K., Itoh,K., Yoshii,J., Yokouchi,H. and Matsubara,K.
              Institute for Molecular and Cellular Biology
              Osaka University
              3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
source        1..27
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="cm1743"
              /clone_lib="Human colon mucosa"
              /note="Adult male, tissue_type = colon mucosa"

BASE COUNT    13 a 5 c 3 g 6 t
ORIGIN

Query Match      0.6%; Score 15.8; DB 10; Length 27;
Best Local Similarity 89.5%; Pred. NO. 1.7e+07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2508 aacacaatggtactcaaaa 2526
      ||||| ||||| |||||
      Db 9 AACACAATGGTATTCCAA 27

RESULT 13
LOCUS      A1826975/c
DEFINITION A1826975 28 bp mRNA linear EST 24-AUG-1999
            WK55a12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419294 3'
            similar to SW:AR34_HUMAN O15144 ARP2/3 COMPLEX 34 KD SUBUNIT ;,
            mRNA sequence.
ACCESSION   A1826975
VERSION     A1826975.1  GI:5447646
KEYWORDS    EST.
SOURCE      Homo sapiens
ORGANISM    Human.
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE       1 (bases 1 to 28)
JOURNAL     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            Cloning by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2419294"

ACCESSION      D25863.1  GI:500531
VERSION        D25863.1
KEYWORDS       EST.
SOURCE         Homo sapiens
ORGANISM       Human.

REFERENCE
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE         Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL       1 (bases 1 to 27)
COMMENT       Global analysis of gene expression in colon mucosa: a large scale
              random cDNA sequencing analysis
              Unpublished (1994)
              Contact: Okubo,K., Itoh,K., Yoshii,J., Yokouchi,H. and Matsubara,K.
              Institute for Molecular and Cellular Biology
              Osaka University
              3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
source        1..27
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="cm1743"
              /clone_lib="Human colon mucosa"
              /note="Adult male, tissue_type = colon mucosa"

BASE COUNT    13 a 5 c 3 g 6 t
ORIGIN

Query Match      0.6%; Score 15.8; DB 10; Length 27;
Best Local Similarity 89.5%; Pred. NO. 1.7e+07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2508 aacacaatggtactcaaaa 2526
      ||||| ||||| |||||
      Db 9 AACACAATGGTATTCCAA 27

RESULT 13
LOCUS      A1826975/c
DEFINITION A1826975 28 bp mRNA linear EST 24-AUG-1999
            WK55a12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419294 3'
            similar to SW:AR34_HUMAN O15144 ARP2/3 COMPLEX 34 KD SUBUNIT ;,
            mRNA sequence.
ACCESSION   A1826975
VERSION     A1826975.1  GI:5447646
KEYWORDS    EST.
SOURCE      Homo sapiens
ORGANISM    Human.
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE       1 (bases 1 to 28)
JOURNAL     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            Cloning by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2419294"

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/clone_lib="NCI_CGAP_Pr22"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT    5 a 5 c 10 g 8 t
ORIGIN

Query Match      0.6%; Score 15.8; DB 9; Length 28;
Best Local Similarity 74.1%; Pred. NO. 1.7e+07;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 330 cagcactactacgacaagtgcaccaag 356
      ||||| ||||| ||||| |||||
      Db 28 CTGCACTACCATCAAGTGCTCAAGG 2

RESULT 14
LOCUS      AZ799395
DEFINITION AZ799395 28 bp DNA linear GSS 16-FEB-2001
            clone UUGC2M0056N16 R, DNA sequence.
ACCESSION   AZ799395
VERSION     AZ799395.1  GI:12950469
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0056 row: N column: 16
              Seq primer: CACACAGGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 28.
              Location/Qualifiers
              1..28
              /organism="Mus musculus"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0056N16"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA

```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 14 c 13 g 1 t
ORIGIN

Query Match 0.6%; Score 15.8; DB 12; Length 28;
Best Local Similarity 74.1%; Pred. No. 1.7e+07;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 17 gggcggggagcactccacccctgccc 43
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Db 2 GGGGGGGGGGGCTCCCCCCCCCCC 28

RESULT 15
AZ475726

LOCUS AZ475726 29 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0294F02F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0294F02 F, DNA sequence.

ACCESSION AZ475726
VERSION AZ475726.1 GI:10633851
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0294 row: F column: 02
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1..29
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/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42hv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

FEATURES
source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 5 c 11 g 3 t
ORIGIN

Query Match 0.6%; Score 15.8; DB 12; Length 29;
Best Local Similarity 74.1%; Pred. No. 1.7e+07;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1715 actcgccaagggtgaagcagagagaataa 1741
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Db 2 AATCGCCAGGGGATGAGCAGAGATAA 28

Search completed: September 7, 2002, 01:05:00
Job time: 5716 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 02:04:54 ; Search time 4642.65 Seconds
(without alignments)
17434.836 Million cell updates/sec

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Perfect score: 3868
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 524256

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_hlg:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
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17: em_hum:*
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33: em_hlgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

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c	3	25	0.6	25	6	AR028694	AR028694 Sequence
c	4	25	0.6	25	6	AR086505	AR086505 Sequence
c	5	23	0.6	23	6	AR028695	AR028695 Sequence
c	6	23	0.6	23	6	AR028696	AR028696 Sequence
c	7	23	0.6	23	6	AR086506	AR086506 Sequence
c	8	23	0.6	23	6	AR086507	AR086507 Sequence
c	9	22	0.6	22	6	AR028698	AR028698 Sequence
c	10	22	0.6	22	6	AR086509	AR086509 Sequence
c	11	21	0.5	21	6	AR028691	AR028691 Sequence
c	12	21	0.5	21	6	AR028692	AR028692 Sequence
c	13	21	0.5	21	6	AR028699	AR028699 Sequence
c	14	21	0.5	21	6	AR086502	AR086502 Sequence
c	15	21	0.5	21	6	AR086503	AR086503 Sequence
c	16	21	0.5	21	6	AR086510	AR086510 Sequence
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c	19	19.8	0.5	24	6	A75929	A75929 Sequence
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c	24	18	0.5	27	6	AR143939	AR143939 Sequence
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c	37	17.4	0.4	30	6	E30025	E30025 Method for
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 9 from patent US 5858753.
ACCESSION AR028693
VERSION AR028693.1 GI:5940666
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid Kinase
JOURNAL Patent: US 5858753-A 9 12-JAN-1999;
FEATURES
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SOURCE 1..26
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION Sequence 9 from patent US 5985589.
ACCESSION AR086504
VERSION AR086504.1 GI:10013270
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid Kinase
JOURNAL Patent: US 5985589-A 9 16-NOV-1999;
FEATURES Location/Qualifiers
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DEFINITION Sequence 10 from patent US 5858753.
ACCESSION AR028694
VERSION AR028694.1 GI:5940667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid Kinase
JOURNAL Patent: US 5858753-A 10 12-JAN-1999;
FEATURES Location/Qualifiers
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BASE COUNT 4 a 9 c 10 g 2 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.4e+06;
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QY 1435 ggcgagctgcccattcctgagcc 1459
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RESULT 4
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DEFINITION Sequence 10 from patent US 5985589.
ACCESSION AR086505
VERSION AR086505.1 GI:10013271

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid Kinase
JOURNAL Patent: US 5985589-A 10 16-NOV-1999;
FEATURES Location/Qualifiers
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DEFINITION Sequence 11 from patent US 5858753.
ACCESSION AR028695
VERSION AR028695.1 GI:5940668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid Kinase
JOURNAL Patent: US 5858753-A 11 12-JAN-1999;
FEATURES Location/Qualifiers
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BASE COUNT 4 a 6 c 10 g 3 t
ORIGIN

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RESULT 6
LOCUS AR028696/c 23 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5858753.
ACCESSION AR028696
VERSION AR028696.1 GI:5940669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid Kinase
JOURNAL Patent: US 5858753-A 12 12-JAN-1999;
FEATURES Location/Qualifiers
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ORIGIN

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|||||
Db 23 CTCTGTGTCCTGTGTGTCCTGG 1

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LOCUS AR086506 23 bp DNA Linear PAT 07-SEP-2000
DEFINITION Sequence 11 from patent US 5985589.
ACCESSION AR086506
VERSION AR086506.1 GI:10013272
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5985589-A 11 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..23
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BASE COUNT 4 a 6 c 10 g 3 t
ORIGIN

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LOCUS AR086507 23 bp DNA Linear PAT 07-SEP-2000
DEFINITION Sequence 12 from patent US 5985589.
ACCESSION AR086507
VERSION AR086507.1 GI:10013273
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5985589-A 12 16-NOV-1999;
FEATURES Location/Qualifiers
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ORIGIN

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
AR028698/c

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DEFINITION Sequence 14 from patent US 5858753.
ACCESSION AR028698
VERSION AR028698.1 GI:5940671
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 14 12-JAN-1999;
FEATURES Location/Qualifiers
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BASE COUNT 5 a 7 c 6 g 4 t
ORIGIN

Query Match 0.6%; Score 22; DB 6; Length 22;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 GGAACGTGCCTCTACATGTG 1

RESULT 10
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DEFINITION Sequence 14 from patent US 5985589.
ACCESSION AR086509
VERSION AR086509.1 GI:10013275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5985589-A 14 16-NOV-1999;
FEATURES Location/Qualifiers
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BASE COUNT 5 a 7 c 6 g 4 t
ORIGIN

Query Match 0.6%; Score 22; DB 6; Length 22;
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Db 22 GGAACGTGCCTCTACATGTG 1

RESULT 11
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DEFINITION Sequence 7 from patent US 5858753.
ACCESSION AR028691
VERSION AR028691.1 GI:5940664
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 7 12-JAN-1999;
FEATURES Location/Qualifiers

source 1..21
 BASE COUNT 5 a 6 c 5 g 5 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.2e+07;
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QY 2557 catgctgacctgcagatgat 2577
 Db 1 CATGCTGACCTGCAGATGAT 21

RESULT 12
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 ACCESSION AR028692
 VERSION AR028692.1 GI:5940665
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
 TITLE Lipid Kinase
 JOURNAL Patent: US 5858753-A 8 12-JAN-1999;
 FEATURES Location/Qualifiers
 source 1..21

BASE COUNT 4 a 9 c 4 g 4 t
 ORIGIN

Query Match 0.5%; Score 21; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;
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QY 2899 ccgagagagtgaggcagctgtt 2919
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 LOCUS AR028699 21 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 16 from patent US 5858753.
 ACCESSION AR028699
 VERSION AR028699.1 GI:5940672
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
 TITLE Lipid Kinase
 JOURNAL Patent: US 5858753-A 16 12-JAN-1999;
 FEATURES Location/Qualifiers
 source 1..21

BASE COUNT 2 a 5 c 5 g 9 t
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 DEFINITION Sequence 7 from patent US 5985589.
 ACCESSION AR086502
 VERSION AR086502.1 GI:10013268
 KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
 TITLE Lipid Kinase
 JOURNAL Patent: US 5985589-A 7 16-NOV-1999;
 FEATURES Location/Qualifiers
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BASE COUNT 5 a 6 c 5 g 5 t
 ORIGIN

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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 CATGCTGACCTGCAGATGAT 21

RESULT 15
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 ACCESSION AR086503
 VERSION AR086503.1 GI:10013269
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
 TITLE Lipid Kinase
 JOURNAL Patent: US 5985589-A 8 16-NOV-1999;
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BASE COUNT 4 a 9 c 4 g 4 t
 ORIGIN

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 Db 21 CCGAGAGAGTGCGCAGCTGTT 1

Search completed: September 7, 2002, 05:22:56
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 03:09:20 : Search time 395.64 Seconds
(without alignments)
16785.525 Million cell updates/sec

Title: US-10-049-743-1
Perfect score: 3868
Sequence: 1 gaattcgagcagcagcgccg.....ggcttgggtacagagattc 3868

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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1662488

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Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	0.7	26	19	AAV31345
2	26	0.7	26	20	AAV15937
3	26	0.7	26	21	AA232887
4	25	0.6	25	19	AAV31346
5	25	0.6	25	20	AAV15938
6	25	0.6	25	21	AA232888
7	23	0.6	23	19	AAV31347
8	23	0.6	23	19	AAV31348
9	23	0.6	23	20	AAV15939

c 10	23	0.6	23	20	AAV15940	Probe used to isol
c 11	23	0.6	23	21	AA232889	Human PI 3-kinase-
c 12	23	0.6	23	21	AA232890	Human PI 3-kinase-
c 13	22	0.6	22	19	AAV31350	Phosphatidylinosit
c 14	22	0.6	22	20	AAV15942	PCR primer used to
c 15	22	0.6	22	21	AA232892	Human PI 3-kinase-
c 16	21.4	0.6	21	19	AAV31343	Polymorphic fragme
c 17	21	0.5	21	19	AAV31344	Phosphatidylinosit
c 18	21	0.5	21	19	AAV31351	Phosphatidylinosit
c 19	21	0.5	21	19	AAV31351	Phosphatidylinosit
c 20	21	0.5	21	20	AAV15935	PCR primer used to
c 21	21	0.5	21	20	AAV15936	PCR primer used to
c 22	21	0.5	21	20	AAV15943	PCR primer used to
c 23	21	0.5	21	21	AA232885	Human PI 3-kinase-
c 24	21	0.5	21	21	AA232886	Human PI 3-kinase-
c 25	21	0.5	21	21	AA232887	Human PI 3-kinase-
c 26	21	0.5	21	21	AA232893	Human PI 3-kinase-
c 27	20	0.5	20	21	AAV3114	PI3K antisense inh
c 28	20	0.5	20	21	AAV3115	PI3K antisense inh
c 29	20	0.5	20	21	AAV3116	PI3K antisense inh
c 30	20	0.5	20	21	AAV3117	PI3K antisense inh
c 31	20	0.5	20	21	AAV3118	PI3K antisense inh
c 32	20	0.5	20	21	AAV3119	PI3K antisense inh
c 33	20	0.5	20	21	AAV3120	PI3K antisense inh
c 34	20	0.5	20	21	AAV3121	PI3K antisense inh
c 35	20	0.5	20	21	AAV3122	PI3K antisense inh
c 36	20	0.5	20	21	AAV3123	PI3K antisense inh
c 37	20	0.5	20	21	AAV3124	PI3K antisense inh
c 38	20	0.5	20	21	AAV3125	PI3K antisense inh
c 39	20	0.5	20	21	AAV3126	PI3K antisense inh
c 40	20	0.5	20	21	AAV3127	PI3K antisense inh
c 41	20	0.5	20	21	AAV3128	PI3K antisense inh
c 42	20	0.5	20	21	AAV3129	PI3K antisense inh
c 43	20	0.5	20	21	AAV3130	PI3K antisense inh
c 44	20	0.5	20	21	AAV3131	PI3K antisense inh
c 45	20	0.5	20	21	AAV3132	PI3K antisense inh

ALIGNMENTS

RESULT 1
AAV31345/c
AAV31345 standard; DNA; 26 BP.
12-OCT-1998 (first entry)
Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.
Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
carcinogenesis; diagnosis; PCR; primer; RACE; ss.
Synthetic.
Homo sapiens.
W09823760-A1.
04-JUN-1998.
25-NOV-1997; 97WO-US21655.
25-NOV-1996; 96US-0777405.
(ICOS-) ICOS CORP.
Chantry DH, Hoekstra MF, Holtzman DA;
WPI; 1998-322736/28.
New phosphatidylinositol 3-kinase catalytic subunit - used to
develop products for modulating kinase activity in immune system

```
PT signalling and in carcinogenesis
XX
XX Example 1; Page 11; 53pp; English.
XX
CC 2 Antisense gene-specific oligonucleotide primers (see AAV31345 and
CC AAV31346) respectively comprise a primary RACE primer and a nested
CC RACE primer, and are based on the 5' end of M#928, a cDNA clone
CC obtained from human macrophage cDNA by PCR amplification (see
CC AAV31343-44). They were used to amplify 5' sequences of human
CC phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic
CC subunit cDNA, using leucocyte cDNA as template. Amplified products
CC were used as templates in a nested PCR and the reamplified products
CC were then analysed using probes (see AAV31347-48) specific for p110
CC delta. The specific 5' RACE PCR products were combined with
CC partial clones #249 and M#928 to produce a composite cDNA (AAV31340)
CC sequence coding for human PI 3-kinase p110 delta catalytic subunit
CC (see AAV58570). This can be used to develop products for modulating
CC PI 3-kinase activity in immune system signalling and in
CC carcinogenesis.
XX
XX Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
SQ

Query Match 0.7%; Score 26; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 gggaagctgcctcacatgagccc 1525
DB 26 GGGAACGCTGCTTACATGTGGCC 1

RESULT 2
AA315937/C
ID .AA315937 standard; DNA: 26 BP.
XX
XX AAX15937:
AC
AC
XX 14-MAY-1999 (first entry)
DT
XX
XX PCR primer used to amplify cDNA sequence encoding p110-delta.
DE
XX
XX Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;
XX PI 3-kinase mediated signalling; immune system; phosphatidylinositol;
XX PI; kinase activity; PCR primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US5882910-A.
XX
XX 16-MAR-1999.
XX
XX 25-NOV-1997; 97US-0977871.
XX
XX 25-NOV-1997; 97US-0977871.
XX
XX 25-NOV-1996; 96US-0777405.
XX
XX (ICOS-) ICOS CORP.
XX
XX Chantry DH, Hoekstra MF, Holtzman DA;
XX
XX WPI; 1999-214067/18.
XX
XX Novel catalytic subunits derived from phosphatidylinositol 3-kinase
XX PT enzymes - useful as antigens and for identifying agents which
XX PT modulate the enzymes kinase activity or binding to substrates and
XX PT co-factors
XX
XX Example 1; Columns 6; 22pp; English.
XX
XX PCR primers AAX15937-38 were used to isolate cDNA encoding a catalytic
XX subunit (p110-delta), derived from a phosphatidylinositol 3-kinase
```

```
CC enzyme which is involved in PI3-Kinase mediated signalling in the
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
CC p110-delta may be used as an antigen in the production of
CC antibodies (using standard techniques) which may be used, for
CC example, to modulate (ie blocking, inhibiting or stimulating) the
CC binding between p110-delta and its binding partner. p110-delta may
CC also be used in assays to identify modulators which inhibit or
CC activate its kinase activity.
XX
XX Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
SQ

Query Match 0.7%; Score 26; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 gggaagctgcctcacatgagccc 1525
DB 26 GGGAACGCTGCTTACATGTGGCC 1

RESULT 3
AA32887/C
ID AA32887 standard; DNA: 26 BP.
XX
XX AA32887:
AC
AC
XX 09-FEB-2000 (first entry)
DT
XX
XX Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #9.
DE
XX
XX Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
XX phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
XX phosphatidylinositol (3, 4, 5) triphosphate; PI3; activation; G protein;
XX cellular response; growth; differentiation; apoptosis;
XX phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
XX Interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
XX antagonist; agonist; treatment; disorder; cell growth.
XX cell differentiation; immune activation; PCR; primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US598589-A.
XX
XX 16-NOV-1999.
XX
XX 06-JAN-1999; 99US-0225951.
XX
XX 25-NOV-1997; 97US-0977871.
XX
XX 25-NOV-1996; 96US-0777405.
XX
XX (ICOS-) ICOS CORP.
XX
XX Holtzman DA, Hoekstra MF, Chantry DH;
XX
XX WPI; 2000-012785/01.
XX
XX Identifying modulators of lipid kinase subunit p110delta activity -
XX
XX Example 1; Column 6; 22pp; English.
XX
XX This sequence represents human p110-delta PCR primer #9, used in the
XX CC generation of a full-length cDNA (AA32882) encoding a novel lipid
XX CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol
XX CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a
XX CC membrane-localising p85 subunit and a catalytic p110 subunit. These
XX CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which
XX CC are differentially expressed, and p110 has to date three isoforms
XX CC (alpha, beta and gamma) that vary in their ability to associate with p85.
XX CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at
XX CC the 3' hydroxyl of the inositol ring with the primary product of PI
```

CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)
CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G
CC proteins and PI 3-kinase activation is believed to be involved in a
CC range of cellular responses including cell growth, differentiation and
CC apoptosis. The downstream targets of the phosphorylated lipids generated
CC following PI 3-kinase activation have not been well characterised,
CC although some isoforms of protein kinase C (PKC) are directly activated
CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain
CC aspects of leukocyte activation, such as Interleukin-2 (IL-2) production
CC in T cells, and leukocyte signalling through G-protein coupled
CC receptors, p110-delta, or nucleotides encoding it, may be used to
CC identify modulators of p110-delta and/or PI 3-kinase activity. These may
CC be useful in the treatment of disorders associated with cell growth,
CC cell differentiation, apoptosis or immune activation.
CC
XX
SQ Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;

Query Match 0.7%; Score 26; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1500 gggaacgtgcctcacatgctgccc 1525
|||||
DB 26 GGGAACGCTGCTCTACATGTGGCCC 1

RESULT 4
AAV31346/C
ID AAV31346 standard; DNA; 25 BP.
XX
AC AAV31346;
XX
DT 12-OCT-1998 (first entry)
XX
XX Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.
DE
XX Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
KW carcinogenesis; diagnosis; PCR; primer; RACE; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN WO9823760-A1.
XX
PD 04-JUN-1998.
XX
PF 25-NOV-1997; 97WO-US21655.
XX
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
PI Chantry DH, Hoekstra MF, Holtzman DA;
XX
XX WPI; 1998-322736/28.
DR
XX
PT New phosphatidylinositol 3-kinase catalytic subunit - used to
PT develop products for modulating kinase activity in immune system
PT signalling and in carcinogenesis
XX
PS Example 1; Page 11; 53pp; English.
XX
CC 2 Antisense gene-specific oligonucleotide primers (see AAV31345 and
CC AAV31346) respectively comprise a primary RACE primer and a nested
CC RACE primer, and are based on the 5' end of M#928, a cDNA clone
CC obtained from human macrophage cDNA by PCR amplification (see
CC AAV31343-44). They were used to amplify 5' sequences of human
CC phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic
CC subunit cDNA, using leucocyte cDNA as template. Amplified products
CC were used as templates in a nested PCR and the reamplified products
CC were then analysed using probes (see AAV31347-48) specific for p110
CC delta. The specific 5' RACE PCR products were combined with

CC partial clones #249 and M#928 to produce a composite cDNA (AAV31340)
CC sequence coding for human PI 3-Kinase p110 delta catalytic subunit
CC (see AAW58570). This can be used to develop products for modulating
CC PI 3-kinase activity in immune system signalling and in
CC carcinogenesis.
XX
SQ Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;

Query Match 0.6%; Score 25; DB 19; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1435 ggcggactgcctccatgctgagcc 1459
|||||
DB 25 GGCGGACTGCCCCCATTTGCTGGGCC 1

RESULT 5
AAV15938/C
ID AAV15938 standard; DNA; 25 BP.
XX
AC AAV15938;
XX
DT 14-MAY-1999 (first entry)
XX
DE PCR primer used to amplify cDNA sequence encoding p110-delta.
DE
XX Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;
KW PI3-kinase mediated signalling; immune system; phosphatidylinositol;
KW PI; kinase activity; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN US5882910-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-0977871.
XX
PR 25-NOV-1997; 97US-0977871.
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
PI Chantry DH, Hoekstra MF, Holtzman DA;
XX
XX WPI; 1999-214067/18.
DR
XX
PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase
PT enzymes - useful as antigens and for identifying agents which
PT modulate the enzymes kinase activity or binding to substrates and
PT co-factors
XX
PS Example 1; Columns 6; 22pp; English.
XX
CC PCR primers AAV15937-38 were used to isolate cDNA encoding a catalytic
CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase
CC enzyme which is involved in PI3-kinase mediated signalling in the
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
CC p110-delta may be used as an antigen in the production of
CC antibodies (using standard techniques) which may be used, for
CC example, to modulate (ie blocking, inhibiting or stimulating) the
CC binding between p110-delta and its binding partner. p110-delta may
CC also be used in assays to identify modulators which inhibit or
CC activate its kinase activity.
XX
SQ Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;

Query Match 0.6%; Score 25; DB 20; Length 25;


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AAV31348/c
ID AAV31348 standard; DNA; 23 BP.
XX
AC AAV31348;
XX
DT 12-OCT-1998 (first entry)
XX
DE Phosphatidylinositol 3-kinase p110 delta subunit probe.
XX
KW Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
KW carcinogenesis; diagnosis; probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9823760-A1.
XX
PD 04-JUN-1998.
XX
PF 25-NOV-1997; 97WO-US21655.
XX
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
XX
PI Chantry DH, Hoekstra MF, Holtzman DA;
XX
DR WPI; 1998-322736/28.
XX
PT New phosphatidylinositol 3-kinase catalytic subunit - used to
PT develop products for modulating kinase activity in immune system
PT signalling and in carcinogenesis
XX
PS Example 1; Page 11; 53pp; English.
XX
CC 2 Oligonucleotide probes (see AAV31347 and AAV31348) are specific for
CC the human phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta
CC catalytic subunit. They were used in Southern blotting to screen
CC clones obtained from 5'RACE and nested PCR amplifications of human
CC leukocyte cDNA (see AAV31345-46). Specific 5'RACE PCR products were
CC identified, and were combined with partial clones #249 and #928 to
CC produce a composite cDNA (AAV31340) sequence coding for human PI
CC 3-kinase p110 delta catalytic subunit (see AAW58570). This can be
CC used to develop products for modulating PI 3-kinase activity in
CC immune system signalling and in carcinogenesis.
XX
SQ Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;

Query Match 0.6%; Score 23; DB 19; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1132 ctcctgtctccctgtgtccctcg 1154
DB 23 CTCTGTGTCCTGTGTGTCCTCG 1

RESULT 9
AAV31348/c
ID AAV31348 standard; DNA; 23 BP.
XX
AC AAV31348;
XX
DT 12-OCT-1998 (first entry)
XX
DE Phosphatidylinositol 3-kinase p110 delta subunit probe.
XX
KW Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
KW carcinogenesis; diagnosis; probe; ss.
XX
OS Synthetic.

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OS Homo sapiens.
XX
PN US5882910-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-0977871.
XX
PR 25-NOV-1997; 97US-0977871.
XX
PA (ICOS-) ICOS CORP.
XX
PI Chantry DH, Hoekstra MF, Holtzman DA;
XX
DR WPI; 1999-214067/18.
XX
PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase
PT enzymes - useful as antigens and for identifying agents which
PT modulate the enzymes kinase activity or binding to substrates and
PT co-factors
XX
PS Example 1; Columns 7; 22pp; English.
XX
CC Probes AAV31340 were used to isolate cDNA encoding a catalytic
CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase
CC enzyme which is involved in PI3-kinase mediated signalling in the
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
CC p110-delta may be used as an antigen in the production of
CC antibodies (using standard techniques) which may be used, for
CC example, to modulate (ie blocking, inhibiting or stimulating) the
CC binding between p110-delta and its binding partner. p110-delta may
CC also be used in assays to identify modulators which inhibit or
CC activate its kinase activity.
XX
SQ Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;

Query Match 0.6%; Score 23; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1149 ccctgagagccgttcgcacac 1171
DB 23 CCCTGAGCAGCCGTTCCGACAC 1

RESULT 10
AAV31348/c
ID AAV31348 standard; DNA; 23 BP.
XX
AC AAV31348;
XX
DT 14-MAY-1999 (first entry)
XX
DE Probe used to isolate cDNA sequence encoding p110-delta.
XX
KW Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;
KW PI3-kinase mediated signalling; immune system; phosphatidylinositol;
KW PI; kinase activity; probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5882910-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-0977871.
XX
PR 25-NOV-1997; 97US-0977871.
XX
PA (ICOS-) ICOS CORP.
XX
PI Chantry DH, Hoekstra MF, Holtzman DA;
XX
DR WPI; 1999-214067/18.
XX
PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase
PT enzymes - useful as antigens and for identifying agents which
PT modulate the enzymes kinase activity or binding to substrates and
PT co-factors
XX
PS Example 1; Columns 7; 22pp; English.
XX
CC Probes AAV31340 were used to isolate cDNA encoding a catalytic
CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase
CC enzyme which is involved in PI3-kinase mediated signalling in the
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
CC p110-delta may be used as an antigen in the production of
CC antibodies (using standard techniques) which may be used, for
CC example, to modulate (ie blocking, inhibiting or stimulating) the
CC binding between p110-delta and its binding partner. p110-delta may
CC also be used in assays to identify modulators which inhibit or
CC activate its kinase activity.
XX
SQ Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;

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XX (ICOS-) ICOS CORP.
PA Chantry DH, Hoekstra MF, Holtzman DA:
PI MPI; 1999-214067/18.
XX
XX Novel catalytic subunits derived from phosphatidylinositol 3-kinase
PT enzymes - useful as antigens and for identifying agents which
PT modulate the enzymes kinase activity or binding to substrates and
PT co-factors
XX
XX Example 1; Columns 7; 22pp; English.
XX
XX Probes AAX15939-40 were used to isolate cDNA encoding a catalytic
CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase
CC enzyme which is involved in PI3-kinase mediated signalling in the
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
CC p110-delta may be used as an antigen in the production of
CC antibodies (using standard techniques) which may be used, for
CC example, to modulate (ie blocking, inhibiting or stimulating) the
CC binding between p110-delta and its binding partner. p110-delta may
CC also be used in assays to identify modulators which inhibit or
CC activate its kinase activity.
XX
SQ Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other:

Query Match      0.6%; Score 23; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1132 cctctgacccctggtgctcctgg 1154
    |||||||
DB 23 CTCTGTCTCTCCCTGTGCTGCTCG 1

RESULT 11
AAZ32889/C
ID AAZ32889 standard; DNA; 23 BP.
XX
XX AAZ32889;
XX
XX 09-FEB-2000 (first entry)
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #11.
XX
XX Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
KW phosphatidylinositol (3, 4, 5) triphosphate; PI3; activation; G protein;
KW cellular response; growth; differentiation; apoptosis;
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
KW antagonist; agonist; treatment; disorder; cell growth;
KW cell differentiation; immune activation; PCR; primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5985589-A.
PN 16-NOV-1999.
XX
XX 06-JAN-1999; 99US-0225951.
PF 25-NOV-1997; 97US-0977871.
PR 25-NOV-1996; 96US-0777405.
XX
XX (ICOS-) ICOS CORP.
PA Holtzman DA, Hoekstra MF, Chantry DH:
PI

```

```

DR MPI; 2000-012785/01.
XX
XX Identifying modulators of lipid kinase subunit p110delta activity -
PT Example 1; Column 7; 22pp; English.
XX
XX
XX This sequence represents human p110-delta PCR primer #11, used in the
CC generation of a full-length cDNA (AAZ32882) encoding a novel lipid
CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol
CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a
CC membrane-localising p85 subunit and a catalytic p110 subunit. These
CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which
CC are differentially expressed, and p110 has to date three isoforms
CC (alpha, beta and gamma) that vary in their ability to associate with p85.
CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at
CC the 3' hydroxyl of the inositol ring with the primary product of PI
CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)
CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G
CC proteins and PI 3-kinase activation is believed to be involved in a
CC range of cellular responses including cell growth, differentiation and
CC apoptosis. The downstream targets of the phosphorylated lipids generated
CC following PI 3-kinase activation have not been well characterised,
CC although some isoforms of protein kinase C (PKC) are directly activated
CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain
CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production
CC in T cells, and leukocyte signalling through G-protein coupled
CC receptors. p110-delta, or nucleotides encoding it, may be used to
CC identify modulators of p110-delta and/or PI 3-kinase activity. These may
CC be useful in the treatment of disorders associated with cell growth,
CC cell differentiation, apoptosis or immune activation.
XX
SQ Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other:

Query Match      0.6%; Score 23; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1149 ccctgagacagccgtccgcac 1171
    |||||||
DB 23 CCCTGACAGCAGCGCTCCGCATC 1

RESULT 12
AAZ32890/C
ID AAZ32890 standard; DNA; 23 BP.
XX
XX AAZ32890;
XX
XX 09-FEB-2000 (first entry)
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #12.
XX
XX Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
KW phosphatidylinositol (3, 4, 5) triphosphate; PI3; activation; G protein;
KW cellular response; growth; differentiation; apoptosis;
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
KW antagonist; agonist; treatment; disorder; cell growth;
KW cell differentiation; immune activation; PCR; primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5985589-A.
PN 16-NOV-1999.
XX
XX 06-JAN-1999; 99US-0225951.
PF 25-NOV-1997; 97US-0977871.
PR 25-NOV-1996; 96US-0777405.
XX
XX

```


xx	(ICOS-) ICOS CORP.
PA	
xx	
PI	Holtzman DA, Hoekstra MF, Chantry DH;
xx	
DR	WPI: 2000-012785/01.
xx	
PI	Identifying modulators of lipid kinase subunit p110delta activity -
xx	
PS	Example 1; Column 7; 22pp; English.
xx	
CC	This sequence represents human p110-delta PCR primer #12, used in the
CC	generation of a full-length cDNA (AA32862) encoding a novel lipid
CC	kinase catalytic subunit, p110-delta, related to phosphatidylinositol
CC	3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a
CC	membrane-localising p85 subunit and a catalytic p110 subunit. These
CC	subunits both have isoforms; p85 has two isoforms (alpha and beta) which
CC	are differentially expressed, and p110 has to date three isoforms
CC	(alpha, beta and gamma) that vary in their ability to associate with p85.
CC	PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at
CC	the 3' hydroxyl of the inositol ring with the primary product of PI
CC	3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)
CC	triphosphate (PIP3). PI 3-kinase is activated by interaction with G
CC	proteins and PI 3-kinase activation is believed to be involved in a
CC	range of cellular responses including cell growth, differentiation and
CC	apoptosis. The downstream targets of the phosphorylated lipids generated
CC	following PI 3-kinase activation have not been well characterised,
CC	although some isoforms of protein kinase C (PKC) are directly activated
CC	by PIP3 in vitro. PI 3-kinase also appears to be involved in certain
CC	aspects of leukocyte activation, such as interleukin-2 (IL-2) production
CC	in T cells, and leukocyte signalling through G-protein coupled
CC	receptors. p110-delta, or nucleotides encoding it, may be used to
CC	identify modulators of p110-delta and/or PI 3-kinase activity. These may
CC	be useful in the treatment of disorders associated with cell growth,
CC	cell differentiation, apoptosis or immune activation.
xx	
SQ	Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
xx	
Query Match	0.6%; Score 23; DB 21; Length 23;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
Oy	1132 ctctgtgtccctgtgtccctcg 1154
DB	23 CTTGTGTCCTCGTGTGTCCTCG 1
xx	
RESULT 13	
AAV31350/C	
ID	AAV31350 standard; DNA: 22 BP.
xx	
AC	AAV31350;
xx	
DT	12-OCT-1998 (first entry)
xx	
DE	Phosphatidylinositol 3-kinase p110 delta subunit primer.
xx	
KW	Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
KW	carcinogenesis; diagnosis; PCR; primer; ss.
xx	
OS	Synthetic.
xx	
OS	Homo sapiens.
xx	
PN	W09823760-A1.
xx	
PD	04-JUN-1998.
xx	
PF	25-NOV-1997; 97WO-US21655.
xx	
PR	25-NOV-1996; 96US-0777405.
xx	
PA	(ICOS-) ICOS CORP.

Pt	Chantry DH, Hoekstra MF, Holtzman DA;
Xx	WPI; 1998-322736/28.
Pt	New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system signalling and in carcinogenesis
Pt	Example 1; Page 12; 53pp; English.
Cc	This 3' primer was used with a 5' primer (see AAV31349) in the PCR amplification of 3'RACE PCR products (see AAV31345-46) of human leukocyte cDNA. The 5' primer includes a 5' BamHI site and sequences that code for a FLAG peptide (see AAW58571) which is recognised by the M2 anti-FLAG monoclonal antibody. The PCR product was combined with restriction fragments of partial clones #249 and M#928 to produce a full-length cDNA (see AAY31347) for the p100 delta catalytic subunit (see AAW58570) of human phosphatidylinositol 3-kinase (PI 3-Kinase). This was incorporated into expression vector pcDNA3, and FLAG-tagged p110 delta was expressed in transfected COS cells. p110 delta can be used to develop products for modulating PI 3-kinase activity in immune system signalling and in carcinogenesis.
Sq	Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
Oy	Query Match 0.6%; Score 22; DB 19; Length 22; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1501 ggaacgtcgccctcacagtgg_1522 22 GGACGCTGCCCTCATGTGC 1
Result 14	
ID	AAAX15942/c
XX	AAAX15942 standard; DNA; 22 BP.
XX	AAXI5942;
Df	14-MAY-1999 (first entry)
DE	PCR primer used to amplify cDNA sequence encoding p110-delta.
Kw	Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase; PI3-kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; PCR primer; ss.
OS	Synthetic.
OS	Homo sapiens.
PN	US5882910-A.
PD	16-MAR-1999.
PF	25-NOV-1997; 97U5-0977871.
PR	25-NOV-1997; 97U5-0977871.
PR	25-NOV-1996; 96U5-0777405.
PA	(ICOS-) ICOS CORP.
PI	Chantry DH, Hoekstra MF, Holtzman DA;
DR	WPI; 1999-214067/18.
Pt	Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and co-factors

XX Example 1: Columns 7: 22pp; English.

CC PCR primers AAX15941-42 were used to isolate cDNA encoding a catalytic
 CC subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase
 CC enzyme which is involved in PI3-Kinase mediated signalling in the
 CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
 CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
 CC p110-delta may be used as an antigen in the production of
 CC antibodies (using standard techniques) which may be used, for
 CC example, to modulate (ie blocking, inhibiting or stimulating) the
 CC binding between p110-delta and its binding partner. p110-delta may
 CC also be used in assays to identify modulators which inhibit or
 CC activate its kinase activity.

SQ Sequence 22 BP: 5 A; 7 C; 6 G; 4 T; 0 other;

Query Match 0.6%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 ggaacgtgcctcatatgtgg 1522
 |||||||||||||||||||||
 DB 22 ggaacgtgcctcatatgtgg 1

RESULT 15
 AA232892/C
 ID AA232892 standard; DNA: 22 BP.

AC AA232892;
 XX
 DT 09-FEB-2000 (first entry)

DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #14.

XX
 KW Lipid kinase: catalytic; subunit; p110-delta; PI 3-kinase;
 KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
 KW phosphatidylinositol (3, 4, 5) triphosphate; PI3; activation; G protein;
 KW cellular response; growth; differentiation; apoptosis;
 KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
 KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
 KW antagonist; agonist; treatment; disorder; cell growth;
 KW cell differentiation; immune activation; PCR; primer; ss.

OS Synthetic.
 OS homo sapiens.

XX US5985589-A.

XX 16-NOV-1999.

XX 06-JAN-1999; 99US-0225951.

XX 25-NOV-1997; 97US-0977871.

XX 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Holtzman DA, Hoekstra MF, Chantry DH;

XX WPI; 2000-012785/01.

XX Identifying modulators of lipid kinase subunit p110delta activity -

XX Example 1; Column 7; 22pp; English.

CC This sequence represents human p110-delta PCR primer #14, used in the
 CC generation of a full-length cDNA (AA232882) encoding a novel lipid
 CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol
 CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a
 CC membrane-localising p85 subunit and a catalytic p110 subunit. These

CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which
 CC are differentially expressed, and p110 has to date three isoforms
 CC (alpha, beta and gamma) that vary in their ability to associate with p85.
 CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at
 CC the 3' hydroxyl of the inositol ring with the primary product of PI at
 CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)
 CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G
 CC proteins and PI 3-kinase activation is believed to be involved in a
 CC range of cellular responses including cell growth, differentiation and
 CC apoptosis. The downstream targets of the phosphorylated lipids generated
 CC following PI 3-kinase activation have not been well characterised,
 CC although some isoforms of protein kinase C (PKC) are directly activated
 CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain
 CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production
 CC in T cells, and leukocyte signalling through G-protein coupled
 CC receptors. p110-delta, or nucleotides encoding it, may be used to
 CC identify modulators of p110-delta and/or PI 3-kinase activity. These may
 CC be useful in the treatment of disorders associated with cell growth,
 CC cell differentiation, apoptosis or immune activation.

SQ Sequence 22 BP: 5 A; 7 C; 6 G; 4 T; 0 other;

Query Match 0.6%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||||||||||||||||||||
 DB 22 ggaacgtgcctcatatgtgg 1

Search completed: September 7, 2002, 05:31:33
 Job time: 8533 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 02:10:19 ; Search time 78.65 seconds
(without alignments)
12080.234 Million cell updates/sec

Title: US-10-049-743-1

Perfect score: 3868
Sequence: 1 gaattcgccagcagcgccg.....ggtcttggtgtagaagattc 3868

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 403436

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCtUS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	0.7	26	2	US-08-777-405A-9
2	26	0.7	26	2	US-08-977-871A-9
3	26	0.7	26	2	US-09-225-951-9
4	25	0.6	25	2	US-08-777-405A-10
5	25	0.6	25	2	US-08-977-871A-10
6	25	0.6	25	2	US-09-225-951-10
7	23	0.6	23	2	US-08-777-405A-11
8	23	0.6	23	2	US-08-777-405A-12
9	23	0.6	23	2	US-08-977-871A-11
10	23	0.6	23	2	US-08-977-871A-12
11	23	0.6	23	2	US-09-225-951-11
12	23	0.6	23	2	US-09-225-951-12
13	22	0.6	22	2	US-08-777-405A-14
14	22	0.6	22	2	US-08-977-871A-14
15	22	0.6	22	2	US-09-225-951-14
16	21	0.5	21	2	US-08-777-405A-7
17	21	0.5	21	2	US-08-777-405A-8
18	21	0.5	21	2	US-08-777-405A-16
19	21	0.5	21	2	US-08-977-871A-7
20	21	0.5	21	2	US-08-977-871A-8
21	21	0.5	21	2	US-08-977-871A-16
22	21	0.5	21	2	US-09-225-951-7
23	21	0.5	21	2	US-09-225-951-8
24	21	0.5	21	2	US-09-225-951-16
25	21	0.5	21	3	US-09-357-070-3
26	20	0.5	20	3	US-09-357-070-8
27	20	0.5	20	3	US-09-357-070-9

28	20	0.5	20	3	US-09-357-070-10	Sequence 10, Appl
29	20	0.5	20	3	US-09-357-070-11	Sequence 11, Appl
30	20	0.5	20	3	US-09-357-070-12	Sequence 12, Appl
31	20	0.5	20	3	US-09-357-070-13	Sequence 13, Appl
32	20	0.5	20	3	US-09-357-070-14	Sequence 14, Appl
33	20	0.5	20	3	US-09-357-070-15	Sequence 15, Appl
34	20	0.5	20	3	US-09-357-070-16	Sequence 16, Appl
35	20	0.5	20	3	US-09-357-070-17	Sequence 17, Appl
36	20	0.5	20	3	US-09-357-070-18	Sequence 18, Appl
37	20	0.5	20	3	US-09-357-070-19	Sequence 19, Appl
38	20	0.5	20	3	US-09-357-070-20	Sequence 20, Appl
39	20	0.5	20	3	US-09-357-070-21	Sequence 21, Appl
40	20	0.5	20	3	US-09-357-070-22	Sequence 22, Appl
41	20	0.5	20	3	US-09-357-070-23	Sequence 23, Appl
42	20	0.5	20	3	US-09-357-070-24	Sequence 24, Appl
43	20	0.5	20	3	US-09-357-070-25	Sequence 25, Appl
44	20	0.5	20	3	US-09-357-070-26	Sequence 26, Appl
45	20	0.5	20	3	US-09-357-070-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-777-405A-9/c
Sequence 9, Application US/08777405A
Patent No. 5858753
GENERAL INFORMATION:
APPLICANT: Chantilly, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-777-405A-9
Query Match 0.7% Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0;
Gy 1500 gggaacgtgcctctacatgtgccc 1525
|||||

Db 26 GGGAACGCTGCTCTACATGTGCCCC 1

RESULT 2
US-08-977-871A-9/C
Sequence 9, Application US/08977871A
Patent No. 5882910
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5882910el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-977-871A-9

Query Match 0.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 gggagcgtgcctctacatgtgcccc 1525
Db 26 GGGAACGCTGCTCTACATGTGCCCC 1

RESULT 3
US-09-225-951-9/C
Sequence 9, Application US/09225951
Patent No. 5985589
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-225-951-9

Query Match 0.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 gggagcgtgcctctacatgtgcccc 1525
Db 26 GGGAACGCTGCTCTACATGTGCCCC 1

RESULT 4
US-08-777-405A-10/C
Sequence 10, Application US/08777405A
Patent No. 5858753
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

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: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 25 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: cDNA
: US-08-777-405A-10

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Query Match      0.6%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1435 ggcggactgccccattgctggcc 1459
      |||||||
Db 25 GCGGACTGCCCATTCCTGGGCC 1

```

```

RESULT 5
US-08-977-871A-10/C
: Sequence 10, Application US/08977871A
: Patent No. 5882910
: GENERAL INFORMATION:
:   APPLICANT: Chantry, David
:   APPLICANT: Hoekstra, Merl F.
:   APPLICANT: Holtzman, Douglas A
:   TITLE OF INVENTION: No. 5882910e1 Lipid Kinase
:   NUMBER OF SEQUENCES: 17
:   CORRESPONDENCE ADDRESS:
:     ADDRESS: Marshall O'Toole Gerstein Murray & Borun
:     STREET: 6300 Sears Tower/233 South Wacker Drive
:     CITY: Chicago
:     STATE: Illinois
:     COUNTRY: USA
:     ZIP: 60606
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: Patentin Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/977,871A
:     FILING DATE:
:   CLASSIFICATION:
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: 08/777,405
:       FILING DATE:
:     ATTORNEY/AGENT INFORMATION:
:       NAME: No. 5882910and, Greta E.
:       REGISTRATION NUMBER: 35,302
:       REFERENCE/DOCKET NUMBER: 27866/33441
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: (312) 474-6300
:       TELEFAX: (312) 474-0448
:       TELEX: 25-3856
:   INFORMATION FOR SEQ ID NO: 10:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 25 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:     MOLECULE TYPE: cDNA
: US-08-977-871A-10

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Query Match      0.6%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 GCGGACTGCCCATTCCTGGGCC 1

```

```

RESULT 6
US-09-225-951-10/C
: Sequence 10, Application US/09225951
: Patent No. 5985589
: GENERAL INFORMATION:
:   APPLICANT: Chantry, David
:   APPLICANT: Hoekstra, Merl F.
:   APPLICANT: Holtzman, Douglas A
:   TITLE OF INVENTION: No. 5985589e1 Lipid Kinase
:   NUMBER OF SEQUENCES: 17
:   CORRESPONDENCE ADDRESS:
:     ADDRESS: Marshall O'Toole Gerstein Murray & Borun
:     STREET: 6300 Sears Tower/233 South Wacker Drive
:     CITY: Chicago
:     STATE: Illinois
:     COUNTRY: USA
:     ZIP: 60606
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: Patentin Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09/225,951
:     FILING DATE:
:   CLASSIFICATION:
:     ATTORNEY/AGENT INFORMATION:
:       NAME: No. 5985589and, Greta E.
:       REGISTRATION NUMBER: 35,302
:       REFERENCE/DOCKET NUMBER: 27866/33441
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: (312) 474-6300
:       TELEFAX: (312) 474-0448
:       TELEX: 25-3856
:   INFORMATION FOR SEQ ID NO: 10:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 25 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:     MOLECULE TYPE: cDNA
: US-09-225-951-10

```

```

Query Match      0.6%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1435 ggcggactgccccattgctggcc 1459
      |||||||
Db 25 GCGGACTGCCCATTCCTGGGCC 1

```

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RESULT 7
US-08-777-405A-11/C
: Sequence 11, Application US/08777405A
: Patent No. 5858753
: GENERAL INFORMATION:
:   APPLICANT: Chantry, David
:   APPLICANT: Hoekstra, Merl F.
:   APPLICANT: Holtzman, Douglas A
:   TITLE OF INVENTION: No. 5858753e1 Lipid Kinase
:   NUMBER OF SEQUENCES: 17
:   CORRESPONDENCE ADDRESS:
:     ADDRESS: Marshall O'Toole Gerstein Murray & Borun
:     STREET: 6300 Sears Tower/233 South Wacker Drive
:     CITY: Chicago
:     STATE: Illinois
:     COUNTRY: USA
:     ZIP: 60606
:   COMPUTER READABLE FORM:

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858753and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-777-405A-11
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DB 23 CCCTGGAGCAGCCGTTCCGCATC 1
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RESULT 8
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; Sequence 12, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858753and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-777-405A-12
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Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 23 CTCCTGTCTCCCTGTGTGCCTCG 1
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RESULT 9
US-08-977-871A-11/C
; Sequence 11, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
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; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
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; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-977-871A-11
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Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 23 CCCTGGAGCAGCCGTTCCGCATC 1
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RESULT 10
US-08-977-871A-12/C
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; Sequence 12, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910e1 Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-977-871A-12

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1132 cctctgtccctgtgtcctgg 1154
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Db 23 cctctgtccctgtgtcctgg 1

RESULT 11
US-09-225-951-11/c
; Sequence 11, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589e1 Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-225-951-11

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 cccttgagcagccgttcgcac 1

RESULT 12
US-09-225-951-12/c
; Sequence 12, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589e1 Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
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; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-225-951-12

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DB 23 CTCTGTGTCCCTGTGTCCTGG 1

RESULT 13
US-08-777-405A-14/C
Sequence 14, Application US/08777405A
Patent No. 5858753

GENERAL INFORMATION:

APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-777-405A-14

Query Match 0.6%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 22 GGAAGCCTCCTCTACATGTGG 1

RESULT 14
US-08-977-871A-14/C
Sequence 14, Application US/08977871A
Patent No. 5882910
GENERAL INFORMATION:
APPLICANT: Chantry, David

APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5882910el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: No. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-977-871A-14

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
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DB 22 GGAAGCCTCCTCTACATGTGG 1

RESULT 15
US-09-225-951-14/C
Sequence 14, Application US/09225951
Patent No. 5985589

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/225,951
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-225-951-14

Query Match 0.6%; Score 22; DB 2; length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 22 GGACGCTGCTCTACATGTG 1

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Job time: 11656 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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3	25	0.6	25	11	US-08-777-405-10			Sequence 10, Appl1	
4	25	0.6	25	13	US-08-977-871-10			Sequence 10, Appl1	
5	23	0.6	23	11	US-08-777-405-11			Sequence 11, Appl1	
6	23	0.6	23	11	US-08-777-405-12			Sequence 12, Appl1	
7	23	0.6	23	13	US-08-977-871-11			Sequence 11, Appl1	
8	23	0.6	23	13	US-08-977-871-12			Sequence 12, Appl1	
9	22	0.6	22	11	US-08-777-405-14			Sequence 14, Appl1	
10	22	0.6	22	13	US-08-977-871-14			Sequence 14, Appl1	
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13	21	0.5	21	11	US-08-777-405-7			Sequence 7, Appl1	
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25	21	0.5	21	74	US-60-350-061-934			Sequence 934, App	
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28	20.2	0.5	25	62	US-60-234-017-521404			Sequence 521404,	
29	20.2	0.5	25	74	US-60-353-987-796246			Sequence 796246,	
30	20	0.5	20	1	PCT-US00-00525-8			Sequence 8, Appl1	
31	20	0.5	20	1	PCT-US00-00525-9			Sequence 9, Appl1	

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C 35 20 0.5 20 1 PCT-US00-00525-13 Sequence 13, Appl
C 36 20 0.5 20 1 PCT-US00-00525-14 Sequence 14, Appl
C 37 20 0.5 20 1 PCT-US00-00525-15 Sequence 15, Appl
C 38 20 0.5 20 1 PCT-US00-00525-16 Sequence 16, Appl
C 39 20 0.5 20 1 PCT-US00-00525-17 Sequence 17, Appl
C 40 20 0.5 20 1 PCT-US00-00525-18 Sequence 18, Appl
C 41 20 0.5 20 1 PCT-US00-00525-19 Sequence 19, Appl
C 42 20 0.5 20 1 PCT-US00-00525-20 Sequence 20, Appl
C 43 20 0.5 20 1 PCT-US00-00525-21 Sequence 21, Appl
C 44 20 0.5 20 1 PCT-US00-00525-22 Sequence 22, Appl
C 45 20 0.5 20 1 PCT-US00-00525-23 Sequence 23, Appl
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ALIGNMENTS

RESULT 1
US-08-777-405-9/c

; Sequence 9, Application US/08777405

; GENERAL INFORMATION:

; APPLICANT: Chantry, David

; APPLICANT: Hoekstra, Merl F.

; APPLICANT: Holtzman, Douglas A

; TITLE OF INVENTION: Novel Lipid Kinase

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

; STREET: 6300 Sears Tower/233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/777,405

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Noland, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/33441

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-08-777-405-9

Query Match 0.7%; Score 26; DB 11; Length 26;
Best local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1500 gggagcgtcgtctacatgtgccc 1525
|||||
DB 26 GGGAGCGCTCCTCTACATGTGCC 1

RESULT 2
US-08-977-871-9/c

```
; Sequence 9, Application US/08977871  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: Novel Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/977,871  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-977-871-9
```

Query Match 0.7%; Score 26; DB 13; Length 26;
Best local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1500 gggagcgtcgtctacatgtgccc 1525
|||||
DB 26 GGGAGCGCTCCTCTACATGTGCC 1

RESULT 3
US-08-777-405-10/c
; Sequence 10, Application US/08777405
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: Novel Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-777-405-10

Query Match 0.6%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 gccgagctgccccattgctggacc 1459
|||||
DB 25 GCGGAGCTGCCCATTCGCTGGGCC 1

RESULT 4
US-08-977-871-10/c
Sequence 10, Application US/08977871

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: Novel Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-977-871-10

Query Match 0.6%; Score 25; DB 13; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1435 gccgagctgccccattgctggacc 1459
|||||
DB 25 GCGGAGCTGCCCATTCGCTGGGCC 1

RESULT 5
US-08-777-405-11/c
Sequence 11, Application US/08777405

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: Novel Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-777-405-11

Query Match 0.6%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 cccctgagcagccgttcgcgacc 1171
|||||
DB 23 CCTGAGACAGCCGTTCCGACATC 1

RESULT 6
US-08-777-405-12/c
Sequence 12, Application US/08777405

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: Novel Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago

Query Match 0.6%; Score 23; DB 13; Length 23;

```
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-777-405-12

Query Match
Best Local Similarity 100.0%; Score 23; DB 11; Length 23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1132 ctctgtgtccctgtgtccctgg 1154
Db 23 ctctgtgtccctgtgtccctgg 1

RESULT 7
US-08-977-871-11/c
Sequence 11, Application US/08977871
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: Novel Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
```

```
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-977-871-11

Query Match
Best Local Similarity 100.0%; Score 23; DB 13; Length 23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1149 ccctgagcagccgttcgcgac 1171
Db 23 ccctgagcagccgttcgcgac 1

RESULT 8
US-08-977-871-12/c
Sequence 12, Application US/08977871
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: Novel Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-977-871-12

Query Match
Best Local Similarity 100.0%; Score 23; DB 13; Length 23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1132 ctctgtgtccctgtgtccctgg 1154
Db 23 ctctgtgtccctgtgtccctgg 1

RESULT 9
US-08-777-405-14/c
Sequence 14, Application US/08777405
```



```
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: Novel Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELE: 25-3856
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-777-405-14

Query Match          0.6%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1501 ggaacgtgcctctacatgttg 1522
|||||
Db 22 ggaacgtgcctctacatgttg 1
```

```
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELE: 25-3856
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-977-871-14

Query Match          0.6%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1501 ggaacgtgcctctacatgttg 1522
|||||
Db 22 ggaacgtgcctctacatgttg 1

RESULT 11
US-09-304-232-73
; Sequence 73, Application US/09304232
; GENERAL INFORMATION:
; APPLICANT: Pan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ALEX19 132
; US-09-304-232-73

Query Match          0.6%; Score 21.4; DB 17; Length 29;
Best Local Similarity 88.0%; Pred. No. 5.4e+06;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2175 tggccctgccttcctccatcct 2199
|||||
Db 1 tggccctgccttcctccatcct 25

RESULT 12
PCT-US00-00525-3/c
; Sequence 3, Application PC/TUS0000525
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF PI3 KINASE P110 DELTA EXPRESSION
; FILE REFERENCE: RTSP-0041
```

;; CURRENT APPLICATION NUMBER: PCT/US00/00525
;; CURRENT FILING DATE: 2000-01-06
;; EARLIER APPLICATION NUMBER: US 09/357,070
;; EARLIER FILING DATE: 1999-07-19
;; NUMBER OF SEQ ID NOS: 47
;; SEQ ID NO: 3
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: PCR Primer
PCT-US00-00525-3

Query Match 0.5%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 agtactgagccgtcttcacaca 377
|||||

DB 21 AGTATGAGCCGCTCTTCACACA 1

RESULT 13
US-08-777-405-7

;; Sequence 7, Application US/08777405
;; GENERAL INFORMATION:
;; APPLICANT: Chantry, David
;; APPLICANT: Hoekstra, Merl F.
;; APPLICANT: Holtzman, Douglas A
;; TITLE OF INVENTION: Novel Lipid Kinase
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
;; STREET: 6300 Sears Tower/233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/777,405
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/33441
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
US-08-777-405-7

Query Match 0.5%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 catgctgaccctgcagatgat 2577
|||||

DB 1 CATGCTGACCCCTGCAGATGAT 21

RESULT 14
US-08-777-405-8/C

;; Sequence 8, Application US/08777405
;; GENERAL INFORMATION:
;; APPLICANT: Chantry, David
;; APPLICANT: Hoekstra, Merl F.
;; APPLICANT: Holtzman, Douglas A
;; TITLE OF INVENTION: Novel Lipid Kinase
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
;; STREET: 6300 Sears Tower/233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/777,405
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/33441
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-777-405-8

Query Match 0.5%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2899 ccgagagatgggcagctgtt 2919
|||||

DB 21 CCGAGAGATGGGCAGCTGTT 1

RESULT 15
US-08-777-405-16/C

;; Sequence 16, Application US/08777405
;; GENERAL INFORMATION:
;; APPLICANT: Chantry, David
;; APPLICANT: Hoekstra, Merl F.
;; APPLICANT: Holtzman, Douglas A
;; TITLE OF INVENTION: Novel Lipid Kinase
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
;; STREET: 6300 Sears Tower/233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-777-405-16

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```

Query Match          0.5%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2712 tcacaagagcacaatgacag 2732
      ||||||||||||||||
Db 21 TCACACAGAGCACAATGACAG 1

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Search completed: September 7, 2002, 06:48:39
 Job time: 12644 sec

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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 04:05:20 ; Search time 644.36 Seconds
(without alignments)
16281.165 Million cell updates/sec

Title: US-10-049-743-1

Perfect score: 3868

Sequence: 1 gaattcgagcagagcgccg.....gtctctggtgtagagaaattc 3868

Scoring table:

IDENTITY_NUC

Searched:

2036664 seqs, 1522705736 residues

Total number of hits satisfying chosen parameters: 888728

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pending_Patents_NA_New:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.8	0.5	25	US-09-396-196G-11682	Sequence 11682, A
2	18.8	0.5	25	US-09-396-196G-47365	Sequence 47365, A
3	18.8	0.5	25	US-09-396-196G-127145	Sequence 127145, A
4	18.8	0.5	30	US-09-380-447A-137	Sequence 137, App
5	18.6	0.5	25	US-09-956-604-110238	Sequence 110238, A
6	18.6	0.5	25	US-09-396-196G-52841	Sequence 52841, A
7	18.2	0.5	25	US-09-396-196G-22583	Sequence 22583, A
8	18.2	0.5	25	US-09-396-196G-47366	Sequence 47366, A
9	18.0	0.5	30	US-10-009-1171-3	Sequence 3, Appli
10	17.8	0.5	22	US-09-544-398A-203	Sequence 203, App
11	17.8	0.5	22	US-09-544-398B-203	Sequence 203, App
12	17.8	0.5	25	US-09-396-196G-22842	Sequence 22842, A
13	17.8	0.5	25	US-09-396-196G-44645	Sequence 44645, A
14	17.8	0.5	25	US-09-396-196G-102323	Sequence 102323, A
15	17.6	0.5	25	US-09-956-604-81730	Sequence 81730, A
16	17.6	0.5	25	US-09-956-604-90553	Sequence 90553, A
17	17.6	0.5	25	US-09-396-196G-1131	Sequence 1131, Ap
18	17.6	0.5	25	US-09-396-196G-11681	Sequence 11681, A
19	17.6	0.5	25	US-09-396-196G-66133	Sequence 66133, A
20	17.6	0.5	25	US-09-396-196G-67635	Sequence 67635, A
21	17.6	0.5	25	US-09-396-196G-70613	Sequence 70613, A
22	17.6	0.5	25	US-09-396-196G-79989	Sequence 79989, A
23	17.6	0.5	25	US-09-396-196G-84193	Sequence 84193, A
24	17.6	0.5	25	US-09-396-196G-95477	Sequence 95477, A
25	17.6	0.5	25	US-09-396-196G-114370	Sequence 114370, A

c	26	17.6	0.5	26	6	US-10-025-806-251	Sequence 251, App
	27	17.4	0.4	25	5	US-09-956-604-51106	Sequence 51106, A
	28	17.4	0.4	25	5	US-09-956-604-51110	Sequence 51110, A
	29	17.4	0.4	25	5	US-09-396-196G-40760	Sequence 40760, A
	30	17.4	0.4	25	5	US-09-396-196G-42255	Sequence 42255, A
	31	17.4	0.4	25	5	US-09-396-196G-42272	Sequence 42272, A
	32	17.2	0.4	22	5	US-09-804-717A-16	Sequence 16, Appl
	33	17.2	0.4	23	5	US-09-693-970A-8	Sequence 8, Appl
	34	17.2	0.4	25	5	US-09-956-604-5847	Sequence 5847, Ap
	35	17.2	0.4	25	5	US-09-956-604-122611	Sequence 122611, A
	36	17.2	0.4	25	5	US-09-956-604-124574	Sequence 124574, A
	37	17.2	0.4	25	5	US-09-396-196G-9391	Sequence 9391, Ap
	38	17.2	0.4	25	5	US-09-396-196G-14744	Sequence 14744, A
	39	17.2	0.4	25	5	US-09-396-196G-34462	Sequence 34462, A
	40	17.2	0.4	25	5	US-09-396-196G-49850	Sequence 49850, A
	41	17.2	0.4	25	5	US-09-396-196G-71621	Sequence 71621, A
	42	17.2	0.4	25	5	US-09-396-196G-77181	Sequence 77181, A
	43	17.2	0.4	25	5	US-09-396-196G-77991	Sequence 77991, A
	44	17.2	0.4	25	5	US-09-396-196G-95478	Sequence 95478, A
	45	17.2	0.4	25	5	US-09-396-196G-115915	Sequence 115915, A

ALIGNMENTS

```
RESULT 1
US-09-396-196G-11682
; Sequence 11682, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11682
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-11682

Query Match      0.5%; Score 19.8; DB 5; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.1e+06;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1139 tccctgtgtccctgagcagcc 1161
DB 1 tcaactgtgtccctgagcagcc 23

RESULT 2
US-09-396-196G-47365
; Sequence 47365, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 47365
;
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-47365
```

```
Query Match          0.5%; Score 18.8; DB 5; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.8e+06;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1607 ctgtcatctgcctgcctccagg 1628
      ||||||| ||||| |||||
Db 3 ctgtcatctgcctgcctccagg 24
```

```
RESULT 3
US-09-396-196G-127145
; Sequence 127145, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127145
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-127145
```

```
Query Match          0.5%; Score 18.8; DB 5; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.8e+06;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 701 ctgcagctggagccctcgctc 722
      ||||||| ||||| |||||
Db 1 ctgcagctggagccctcgctc 22
```

```
RESULT 4
US-09-380-447A-137
; Sequence 137, Application US/09380447A
; GENERAL INFORMATION:
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Weiss, Gregory A.
; APPLICANT: Weiss, James A.
; TITLE OF INVENTION: IMPROVEMENTS IN PHAGE DISPLAY
; FILE REFERENCE: P15812
; CURRENT APPLICATION NUMBER: US/09/380,447A
; CURRENT FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 60/134,870
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/133,296
; PRIOR FILING DATE: 1999-05-10
; PRIOR APPLICATION NUMBER: US 60/103,514
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/094,291
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: PCT/USUS99/16596
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 287
; SEQ ID NO 137
; LENGTH: 30
; TYPE: DNA
```

```
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: linker oligonucleotide
US-09-380-447A-137
```

```
Query Match          0.5%; Score 18.8; DB 5; Length 30;
Best Local Similarity 76.7%; Pred. No. 1.8e+06;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
OY 614 cgcgcgaagatgccaattctgcggag 643
      ||||||| ||||| |||||
Db 1 cgcgcgaagatgccaattctgcggag 30
```

```
RESULT 5
US-09-956-604-110238
; Sequence 110238, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; APPLICANT: David Mack
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110238
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-110238
```

```
Query Match          0.5%; Score 18.6; DB 5; Length 25;
Best Local Similarity 84.0%; Pred. No. 2e+06;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 454 acgcgcctcgtgtgacgtgaccc 478
      ||||||| ||||| |||||
Db 1 actgcgtcgtgtgacgcgcgcgc 25
```

```
RESULT 6
US-09-396-196G-52841
; Sequence 52841, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52841
```

```
Query Match          0.5%; Score 18.6; DB 5; Length 25;
Best Local Similarity 84.0%; Pred. No. 2e+06;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 3127 cttgcctgatgcggcgccaggc 3151
      ||||||| ||||| |||||
```

Db 1 ctgtgcctcatgctgcgtcttcacgac 25

RESULT 7

US-09-396-196G-22583/c
; Sequence 22583, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-22583

Query Match

0.5%; Score 18.2; DB 5; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.4e+06;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1983 ccataagtcgtcgcggaactg 2005
||||| ||| | ||| |

Db 24 CCATCAGTCCCTCTGCCAACTG 2

RESULT 8

US-09-396-196G-47366
; Sequence 47366, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47366
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-47366

Query Match

0.5%; Score 18.2; DB 5; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.4e+06;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1608 tgcatactgcctgcgcgagtg 1630
||||| ||| | ||| |

Db 1 tgcatactgcctgcgcgagtg 23

RESULT 9

US-10-009-171-3
; Sequence 3, Application US/10009171
; GENERAL INFORMATION:
; APPLICANT: Andrew LEVER
; APPLICANT: Jane GREATOREX

; APPLICANT: Ramon MCCANN
; APPLICANT: Preetha BALAN

; TITLE OF INVENTION: SIV-BASED PACKAGING-DEFICIENT VECTORS
; FILE REFERENCE: 117-372 / N79496C
; CURRENT APPLICATION NUMBER: US/10/009,171
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: PCT/GB00/02263
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: GB 9916911.2
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: GB 9913459.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: MS Word
; SEQ ID NO 3
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic oligonucleotide
US-10-009-171-3

Query Match

0.5%; Score 18; DB 6; Length 30;
Best Local Similarity 80.8%; Pred. No. 2.6e+06;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1419 agaagaagtcacagaagcgagctgc 1444
||||| ||| | ||| |

Db 5 agaagaagtcacacacagcgagctgc 30

RESULT 10

US-09-544-398A-203
; Sequence 203, Application US/09544398A
; GENERAL INFORMATION:
; APPLICANT: Carnelli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398A-203

Query Match

0.5%; Score 17.8; DB 5; Length 22;
Best Local Similarity 90.5%; Pred. No. 2.8e+06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 103 agcatcttaatcgtcagc 123
||||| ||| | ||| |

Db 1 agcatcttaatgtgtcagc 21

RESULT 11

US-09-544-398B-203
; Sequence 203, Application US/09544398B
; GENERAL INFORMATION:

```

; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-203
```

```

Query Match          0.5%; Score 17.8; DB 5; Length 22;
Best Local Similarity 90.5%; Pred. No. 2.8e+06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 103 agcattcttaatcgcagc 123
|||||
```

```
Db 1 agcattcttaatgltcagc 21
|||||
```

```

RESULT 12
US-09-396-196G-22842/C
; Sequence 22842, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-22842
```

```

Query Match          0.5%; Score 17.8; DB 5; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3779 tctgcagctcccccagagc 3799
|||||
```

```
Db 22 TCTGCGTATCCCGAGCAGC 2
|||||
```

```

RESULT 13
US-09-396-196G-44645/C
; Sequence 44645, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
```

```

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44645
```

```

Query Match          0.5%; Score 17.8; DB 5; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1277 tctgcagctcccccagagc 1297
|||||
```

```
Db 23 TCAGAGTGAGCTGTGCTCG 3
|||||
```

```

RESULT 14
US-09-396-196G-102323
; Sequence 102323, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102323
```

```

Query Match          0.5%; Score 17.8; DB 5; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1849 ggtcaccaagtggaacaaga 1869
|||||
```

```
Db 2 ggtcaccaatggggaacaaga 22
|||||
```

```

RESULT 15
US-09-956-604-81730
; Sequence 81730, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81730
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-81730
```


Query Match 0.5%; Score 17.6; DB 5; Length 25;
 Best Local Similarity 83.3%; Pred. No. 3.1e+06;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2972 aaccgagacgtgtccatcaltc 2995
 ||||| || ||||| |||||
 Db 1 aaccgagacgtgtccatcaltc 24

Search completed: September 7, 2002, 06:59:45
 Job time: 10465 sec

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/organism="Homo sapiens"
/db_xref="GDB:491920"
/db_xref="taxon:9606"
/clone_image="71023"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector: ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3'
adaptor sequence: 5' CTCAGCTTTT TTTT TTTT 3'"
* BASE COUNT
4 a 7 c 11 g 6 t
ORIGIN

Query Match
Best Local Similarity 84.6%; Pred. No. 4.8e+06; Length 28;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1204 cgagcgatgaagctggtgctgag 1229
||||| ||||| ||||| |||||
Db 2 CGAGCGGTCAGCAGCTGCTCTCAGC 27

RESULT 2
BM399411 30 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-57-E01.t.1 Chllocoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM399411
VERSION BM399411.1 GI:18199464
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila.
REFERENCE 1 (bases 1 to 30)
AUTHORS Turkewitz,A.P., Karrier,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
unpublished (2002)
TITLE Contact: Turkewitz AP
JOURNAL Molecular Genetics and Cell Biology
COMMENT University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
source
1..30
Location/Qualifiers
/organism="Tetrahymena thermophila"
/db_xref="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chllocoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK-; Details on library
preparation can be found in Chllocoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT
4 a 10 c 12 g 4 t
ORIGIN

Query Match
Best Local Similarity 84.0%; Pred. No. 7.5e+06; Length 30;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 719 gctcaacctggggcctgtatccc 743
||||| ||||| ||||| |||||
Db 6 GCTCAGCGCTGCGGCGCGTACCC 30

RESULT 3

/organism="Homo sapiens"
/db_xref="GDB:491920"
/db_xref="taxon:9606"
/clone_image="71023"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector: ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3'
adaptor sequence: 5' CTCAGCTTTT TTTT TTTT 3'"
* BASE COUNT
4 a 7 c 11 g 6 t
ORIGIN

AL584657 28 bp mRNA linear EST 28-FEB-2001
LOCUS AL584657
DEFINITION Gallus gallus cDNA clone ROS012612, mRNA sequence.
ACCESSION AL584657
VERSION AL584657.1 GI:13163388
KEYWORDS EST.
SOURCE chicken.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Murray,F.
TITLE Stratagene Chick Embryo Lambda cDNA Library
JOURNAL Unpublished (2001)
COMMENT Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
Seq primer: T3.
FEATURES
source
1..28
Location/Qualifiers
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS012612"
/clone_lib="Stratagene Chick Embryo Lambda cDNA Library (*
937405)"
/tissue_type="Embryo"
/dev_stage="5 days old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Cloned unidirectionally. Primer: Oligo dt. Uni-ZAP XR
vector. Average insert size: 1.5kb.; 5' adaptor sequence:
5' GAATTCGGCAGCAG 3'; 3' adaptor sequence: 5'
CTCAGCTTTT TTTT TTTT 3'"
BASE COUNT
8 a 7 c 11 g 2 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 9.7e+06; Length 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gaattcgagcagcgcgc 18
||||| ||||| ||||| |||||
Db 1 GAATTCGGCAGCAGCGCC 18

RESULT 4
AZ479681/c 26 bp DNA linear GSS 04-OCT-2000
LOCUS AZ479681
DEFINITION IM0300G02R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGIM0300G02 R, DNA sequence.
ACCESSION AZ479681
VERSION AZ479681.1 GI:10639845
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
```

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0300 row: G column: 02
 Seq primer: CACACGAGAAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

Location/Qualifiers

1..26
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0300G02"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 0 c 13 g 0 t

ORIGIN

Query Match

Best Local Similarity 90.0%; Score 16.8; DB 12; Length 26;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3110 cttctctctcctcactctt 3129

Db 26 cttctctcctcctcctcctt 7

RESULT 5

AZ780072

LOCUS 26 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0017H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0017H04 F, DNA sequence.

ACCESSION AZ780072

VERSION AZ780072.1 GI:12911368

KEYWORDS GSS.

SOURCE mouse mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0017 row: H column: 04
 Seq primer: CGTTGTAAACGACGCCACG
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

Location/Qualifiers

1..26
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0017H04"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 6 c 6 g 6 t

ORIGIN

Query Match

Best Local Similarity 90.0%; Score 16.8; DB 12; Length 26;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2851 cacatgtctgtggcattg 2870

Db 1 CACATATGCTCTGGGATTG 20

RESULT 6

AA973948 28 bp mRNA linear EST 23-JUL-1998

LOCUS AA973948/c

DEFINITION oq12802.s1 NCI_CGAP_G4 Homo sapiens cDNA clone IMAGE:1586115 3'

similar to TR:035787 035787 KINESIN-RELATEDD PROTEIN.; mRNA

sequence.

ACCESSION AA973948

VERSION AA973948.1 GI:3149128

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 28)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA library preparation: M. Bento Soares, Ph.D.
CDNA library arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/INL at:
www-bio.linnl.gov/dbip/image/image.html

FEATURES

Trace considered overall poor quality
Insert length: 790 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

1.28

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1586115"
/clone_1id="NCI_CGAP-GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/vector="pVR73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pVR73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "

```

BASE COUNT
ORIGIN

Query Match	0.4%	Score 16.8	DB 9	Length 28
Best Local Similarity	75.0%	Pred. No. 1.6e+07		
Matches	21	Conservative	0	Mismatches 7; Indels 0; Gaps 0;
Oy	3164	agcctgcctccaaagacatccagttatctca	3191	
Db	28	acctctctacattgacatccagagacctca	1	

RESULT

BM398517	30 bp	mRNA	linear	EST 17-JAN-2007
LOCUS	BM398517			
DEFINITION	5009-0-46-D07.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.			

ACCESSION

VERSION	GM:181985/0
KEYWORDS	BM39851/.1
SOURCE	EST.
	Tetrahymena thermophila.

ORGANISATION

REFERENCE
1 (bases 1 to 30)

AUTHORS

TITLE	J. and Klobutcher, L.
JOURNAL	EST from <i>Tetrahymena thermophila</i> , strain CU428.1, growing cells
COMMENT	Unpublished (2002)
	Contact: Turkewitz AP
	USA 3-011-913-3500

University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apcurekew@midway.uchicago.edu
Seq primer: T3.

FEATURES

SOURCE

```
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
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/clone.lib="chicoat/turkewitz cdna (large fraction)"
/note="Vector: Bluescript2 SK⁺; Details on library
preparation can be found in Chicoat and Turkewitz (2000).
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
ORIGIN

Query Match	0.4%;	Score 16.8;	DB 10;	Length 30;
Best Local Similarity	75.0%;	Pred. No. 1.7e+07;		
Matches 21; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

QY 715

```

QY      715 ctgcgtcaaacctggggcctgtacc 74
          || ||||| | ||||| |||||
Db      3  CTGAGCTACGCGGGGGGCCCGGTACC 30

```

RESULT

LOCUS	AZ404206	27 bp	DNA	linear	GSS 03-OCT-2000
DEFINITION	JM0172120F Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0172120 F, DNA sequence.				

ACCESSION

VERSION	AZ404206.1	GI:10528213
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

ORGANISM

REFERENCE
AUTHORS

1 (pages 1 to 27)

Dunn, D., Aoyagi, A., Barber, M., Beaorn, T., Duval, B., Hamll, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.

REFERENCE AUTHORS

TITLE	Mouse whole genome scaffolding with paired end reads from 10x
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0172 row: I column: 20
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

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source
1. .2/
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MUGCM0172120"
/clone_lib="Mouse 10kb plasmid MUGCM library"
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`/lab_host="E. coli strain XL10-Gold, 11-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource`

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (9111473211419b) (AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 0 a 9 c 9 g 9 t
ORIGIN

Query Match 0.4%; Score 16.6; DB 12; Length 27;
Best Local Similarity 82.6%; Pred. No. 1.8e+07;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2030 ctgctgcagctgctgcagctgct 2052

Db 1 CTGCTGCTGCTGCTGCTGCTCT 23

RESULT 9
A2789420/c

LOCUS 29 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M003J11F Mouse 10kb plasmid U06C1M library Mus musculus genomic
clone U06C2M003J11 F, DNA sequence.

ACCESSION A2789420

VERSION A2789420.1 GI:12930223

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: J column: 11
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends

High quality sequence stop: 29.
Location/Qualifiers

1. .29
Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U06C2M003J11"

/clone_lib="Mouse 10kb plasmid U06C1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321141gb1AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 8 a 7 c 6 g 8 t
ORIGIN

Query Match 0.4%; Score 16.4; DB 12; Length 29;
Best Local Similarity 76.9%; Pred. No. 2e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3249 agttaacgaagccctccgtgagagc 3274

Db 26 AGTTAAGGATGACATCCATCAGAC 1

RESULT 10
A2840149

LOCUS 30 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0136M06R Mouse 10kb plasmid U06C1M library Mus musculus genomic
clone U06C2M0136M06 R, DNA sequence.

ACCESSION A2840149

VERSION A2840149.1 GI:13010057

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0136 row: M column: 06
Seq primer: CACACAGGAACACGTATGAC
Class: plasmid ends

High quality sequence stop: 30.
Location/Qualifiers

1. .30
Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U06C2M0136M06"

/clone_lib="Mouse 10kb plasmid U06C1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

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 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0076 row: C column: 04
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers
 1..30
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0076C04"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 4 a 4 c 12 g 10 t

Query Match 0.4%; Score 16.2; DB 12; Length 30;
 Best Local Similarity 72.4%; Pred. No. 2.2e+07;
 Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1088 aaaccgctgcaaacaccctccatcc 1116
 ||||| ||||| ||||| ||||| ||
 Db 30 AACCCAGGTCCATACACGACATAC 2

RESULT 14
 AA601864/c 30 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION IM0420P16 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0420P16 F, DNA sequence.
 ACCESSION AA601864
 VERSION AA601864.1 GI:11724054
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0420 row: P column: 16
 Seq primer: CGTGTAAACGACGCCGACG
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers
 1..30
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0420P16"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 8 a 3 c 11 g 8 t

Query Match 0.4%; Score 16.2; DB 12; Length 30;
 Best Local Similarity 72.4%; Pred. No. 2.2e+07;
 Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2983 tgtccatctacatctcactcagcttg 3011
 ||||| ||||| ||||| ||||| ||
 Db 29 TGTCCATGATCCATCAACACACATG 1

RESULT 15
 AA766400/c 25 bp mRNA linear EST 08-FEB-1998
 LOCUS
 DEFINITION aa36e03.s1 NCI-CGAP-GCB1 Homo sapiens cDNA clone IMAGE:1307068 3',
 similar to TR:Q16342 Q16342 PDCD2=PROGRAMMED CELL DEATH-2/RP8
 HOMOLOG. ;, mRNA sequence.
 ACCESSION AA766400
 VERSION AA766400.1 GI:2817638
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 25)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.

